

# SEARCH REQUEST FORM

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Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

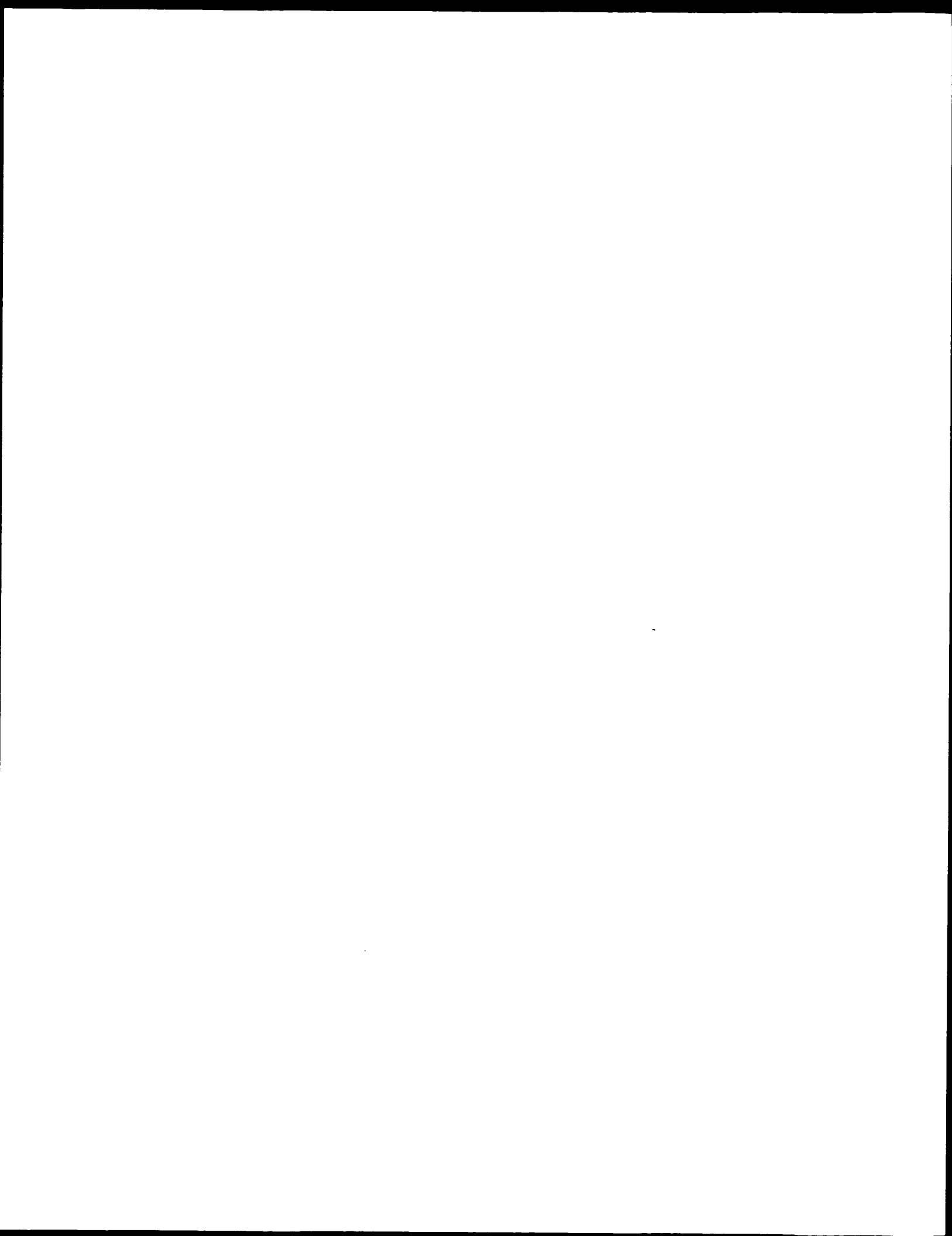
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Number of Databases: 1

Search Site  
\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
Type of Search  
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\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
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\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
☒ Other CGN





PR 25-MAR-1998; 98US-0079294.  
PR 26-MAR-1998; 98US-0079656.  
PR 27-MAR-1998; 98US-0079663.  
PR 27-MAR-1998; 98US-0079664.  
PR 27-MAR-1998; 98US-0079689.  
PR 27-MAR-1998; 98US-0079728.  
PR 27-MAR-1998; 98US-0079786.  
PR 30-MAR-1998; 98US-0079920.  
PR 30-MAR-1998; 98US-0079923.  
PR 31-MAR-1998; 98US-0080105.  
PR 31-MAR-1998; 98US-0080107.  
PR 31-MAR-1998; 98US-0080165.  
PR 31-MAR-1998; 98US-0080194.  
PR 01-APR-1998; 98US-0080327.  
PR 01-APR-1998; 98US-0080328.  
PR 01-APR-1998; 98US-0080333.  
PR 01-APR-1998; 98US-0080334.  
PR 08-APR-1998; 98US-0081049.  
PR 08-APR-1998; 98US-0081070.  
PR 09-APR-1998; 98US-0081071.  
PR 09-APR-1998; 98US-0081195.  
PR 09-APR-1998; 98US-0081203.  
PR 09-APR-1998; 98US-0081229.  
PR 15-APR-1998; 98US-0081817.  
PR 15-APR-1998; 98US-0081838.  
PR 15-APR-1998; 98US-0081952.  
PR 15-APR-1998; 98US-0081955.  
PR 15-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082569.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082704.  
PR 22-APR-1998; 98US-0082804.  
PR 23-APR-1998; 98US-0082767.  
PR 23-APR-1998; 98US-0082796.  
PR 27-APR-1998; 98US-0083336.  
PR 28-APR-1998; 98US-0083322.  
PR 29-APR-1998; 98US-0083392.  
PR 29-APR-1998; 98US-0083495.  
PR 29-APR-1998; 98US-0083496.  
PR 29-APR-1998; 98US-0083499.  
PR 29-APR-1998; 98US-0083500.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083554.  
PR 29-APR-1998; 98US-0083558.  
PR 29-APR-1998; 98US-0083559.  
PR 30-APR-1998; 98US-0083742.  
PR 05-MAY-1998; 98US-0084366.  
PR 06-MAY-1998; 98US-0084414.  
PR 06-MAY-1998; 98US-0084441.  
PR 07-MAY-1998; 98US-0084598.  
PR 07-MAY-1998; 98US-0084600.  
PR 07-MAY-1998; 98US-0084627.  
PR 07-MAY-1998; 98US-0084637.  
PR 07-MAY-1998; 98US-0084639.  
PR 07-MAY-1998; 98US-0084640.  
PR 07-MAY-1998; 98US-0084643.  
PR 13-MAY-1998; 98US-0085323.  
PR 13-MAY-1998; 98US-0085338.  
PR 13-MAY-1998; 98US-0085339.  
PR 15-MAY-1998; 98US-0085573.  
PR 15-MAY-1998; 98US-0085579.  
PR 15-MAY-1998; 98US-0085580.  
PR 15-MAY-1998; 98US-0085582.  
PR 15-MAY-1998; 98US-0085689.  
PR 15-MAY-1998; 98US-0085697.  
PR 15-MAY-1998; 98US-0085700.  
PR 15-MAY-1998; 98US-0085704.  
PR 18-MAY-1998; 98US-0086023.  
PR 22-MAY-1998; 98US-0086392.  
PR 22-MAY-1998; 98US-0086414.  
PR 22-MAY-1998; 98US-0086430.  
PR 22-MAY-1998; 98US-0086486.  
PR 26-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.  
PR 28-MAY-1998; 98US-0087208.  
PR 30-JUL-1998; 98US-0094651.  
PR 11-SEP-1998; 98US-0100038.  
XX (GETH ) GENENTECH INC.  
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX WPI; 1999-551358/46.  
XX N-PSDB; AAZ34313.  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders -  
XX  
XX Claim 12; Fig 217; 530pp; English.  
XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as  
CC sources of probes, primers, for chromosome mapping, and for generation  
CC of antisense sequences. They can also be used to create transgenic  
CC animals. The proteins can be used to treat a variety of diseases and  
CC disorders depending on their function. Diseases that may be treated  
CC include blood coagulation disorders, cancers and cellular adhesion  
CC disorders. They may also be used to raise antibodies. AAZ33891 to  
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and  
CC polypeptide sequence given in the exemplification of the present  
XX invention.  
XX  
SQ Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 20; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1e-94;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSQEVLLMVLVAVGTEHAYRPPRRVCAVRAHGDVPSFVQRYVQPLTTCGHR 60  
DB 1 MRSQEVLLMVLVAVGTEHAYRPPRRVCAVRAHGDVPSFVQRYVQPLTTCGHR 60  
QY 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGWKRTSLPGACGAAICOPPCRNNGSCVQP 120  
DB 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGWKRTSLPGACGAAICOPPCRNNGSCVQP 120  
QY 121 GRCPCPAGWRGTCQSDVDECSARRGGCPQRCVNTAGSYWCQCEHSLSDGTLCPKPG 180  
DB 121 GRCPCPAGWRGTCQSDVDECSARRGGCPQRCVNTAGSYWCQCEHSLSDGTLCPKPG 180  
QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAHLASQALEHGLPDPGSL 240  
DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAHLASQALEHGLPDPGSL 240  
QY 241 VHSFQQLGRIDSLSEIQISFLEQLGSCCKKDS 273  
DB 241 VHSFQQLGRIDSLSEIQISFLEQLGSCCKKDS 273

RESULT 2  
AAW88181  
ID AAW8838 standard; Protein; 273 AA.  
XX AAW88981;  
AC AAW88981;  
XX  
DT 26-APR-1999 (first entry)  
XX Human neuro-growth factor-like protein Zneul.  
XX Zneu-1; neuro-growth factor-like protein; human; breast cancer;  
KW glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;  
KW nerve regeneration; haematopoiesis; fertility; contraception;  
KW antibody.  
XX  
OS Homo sapiens.



XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "putative signal peptide"  
 FT Protein 20..273  
 FT /note= "mature protein"  
 FT Domain 20..104  
 FT /note= "hydrophilic domain (HSM1), homologous to an HSMC3WSA domain"  
 FT Domain 105..135  
 FT /note= "epidermal growth factor-like domain 1"  
 FT Domain 136..177  
 FT /note= "epidermal growth factor-like domain 2"  
 FT Domain 178..273  
 FT /note= "domain HSM2 homologous to an HSMC3WSA domain"  
 PN MO9857983-A2.  
 XX 23-DEC-1998.  
 XX 18-FEB-1998; 98MO-US12763.  
 XX 18-JUN-1997; 97US-0878323.  
 XX 18-JUN-1997; 97US-0050143.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Blumberg H, Jelinek LJ, Lehnert JM, Sheppard PO; Whitmore TE;  
 XX WPI; 1999-095324/08.  
 XX N-PSDB; AAV84341.  
 XX New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells  
 PT Claim 6; Page 47-48; 70pp; English.  
 XX This polypeptide comprises human Zneul, a new neuro-growth factor-like protein. Its amino acid sequence was deduced from the cDNA sequence (see AAV84341) of a cDNA clone isolated from a brain cDNA library. Zneul's closest human homologous is HSMC3WSA, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologous to Notch 4 in its BGF-like domains and may be involved in EGF receptor pathways.  
 CC Zneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thymoid, spinal cord and lymph node. Zneul polypeptide can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thymoid and lymph nodes. It may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Zneul polypeptides (see also AAV8382-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.  
 XX Sequence 273 AA;  
 XX  
 Query Match 100.0%; Score 1505; DB 20; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GRCRCPAGRGDTQSDVDDECSARRGGCPGRCVNTAGSYWCQMEGHSLSADGTLCPVPGK 180  
 DB 121 GRCRCPAGRGDTQSDVDDECSARRGGCPGRCVNTAGSYWCQMEGHSLSADGTLCPVPGK 180  
 QY 181 GPERVAPNPTGVDSAMKEEYORLQSRVDLLEKILQVLAAPHLSASQALEHGLPDPSSL 240  
 DB 181 GPERVAPNPTGVDSAMKEEYORLQSRVDLLEKILQVLAAPHLSASQALEHGLPDPSSL 240  
 QY 241 VHSFQOLGRIDSLSEQISFLEEQLSGSCCKKDS 273  
 DB 241 VHSFQOLGRIDSLSEQISFLEEQLSGSCCKKDS 273  
 RESULT 3  
 AAB44327  
 ID AAB44327 standard; Protein: 273 AA.  
 AC AAB44327;  
 DT 08-FEB-2001 (first entry)  
 DE Human PRO1449 protein sequence SEQ ID NO:510.  
 XX Human, secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 KW expressed sequence tag; detection; cancer.  
 XX Homo sapiens.  
 XX MO200053756-A2.  
 XX 14-SEP-2000.  
 XX 18-FEB-2000; 2000MO-US04341.  
 XX 08-MAR-1999; 99MO-US05028.  
 XX 12-MAR-1999; 99US-0123957.  
 XX 29-MAR-1999; 99US-0126773.  
 XX 21-APR-1999; 99US-0130232.  
 XX 28-APR-1999; 99US-0131445.  
 XX 14-MAY-1999; 99US-0134287.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 29-OCT-1999; 99US-0162506.  
 XX 30-NOV-1999; 99MO-US28313.  
 XX 02-DEC-1999; 99MO-US28551.  
 XX 16-DEC-1999; 99MO-US28555.  
 XX 30-DEC-1999; 99MO-US31243.  
 XX 30-DEC-1999; 99MO-US31274.  
 XX 05-JAN-2000; 2000MO-US00219.  
 XX 06-JAN-2000; 2000MO-US00277.  
 XX 06-JAN-2000; 2000MO-US00376.  
 XX (GENTH) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski FO, Grimaldi CJ, Gurney AU, Hillan KJ;  
 PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI; 2000-611443/58.  
 XX N-PSDB; AAC78587.  
 FT Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PS cellular activities -  
 XX Claim 12; Fig 217; 636pp; English.  
 XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO

CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQVYQFLLTCDGHR 60  
 Db 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQVYQFLLTCDGHR 60  
 QY 61 ACSTYRTIYRTAYRRSPGLAPARYACCPGWKRTSGLPAGCGAAICQPPCRNGGSCVQP 120  
 Db 61 ACSTYRTIYRTAYRRSPGLAPARYACCPGWKRTSGLPAGCGAAICQPPCRNGGSCVQP 120  
 QY 121 GRRCPCAGWRGDTQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPVK 180  
 Db 121 GRRCPCAGWRGDTQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPVK 180  
 QY 181 GPPRVAPNPTGVDKAMKEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
 Db 181 GPPRVAPNPTGVDKAMKEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
 QY 241 VHSFQQLGRIDSLSQISFLEQLGSCCKXDS 273  
 Db 241 VHSFQQLGRIDSLSQISFLEQLGSCCKXDS 273

RESULT 4

AAB18675

ID AAB18675 standard; Protein; 273 AA.

AC AAB18675;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of a human a PRO1449 polypeptide.

XX Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO213; PRO1449;  
 KW angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;  
 KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
 KW arteriosclerosis; cardiac hypertrophy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "signal sequence"

FT Modified-site 19..25

FT /note= "N-myristoylation site"

FT Modified-site 26..30

FT /note= "amidation site"

FT Modified-site 78..84

FT /note= "N-myristoylation site"

FT Modified-site 93..97

FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 97..103

FT /note= "N-myristoylation site"

FT Modified-site 100..106

FT /note= "N-myristoylation site"

FT Modified-site 103..109

FT /note= "N-myristoylation site"

FT 123..135

FT Region /note= "EGF-like domain cysteine pattern signature"  
 FT 130..133  
 FT /note= "cell attachment sequence"  
 FT Modified-site 152..164  
 FT /note= "aspartic acid and asparagine hydroxylation site"  
 FT Modified-site 157..163  
 FT /note= "N-myristoylation site"  
 FT Modified-site 191..197  
 FT /note= "N-myristoylation site"  
 FT Modified-site 265..271  
 FT /note= "N-myristoylation site"

XX W0200053752-A2.

XX 14-SEP-2000.

XX 30-DEC-1999; 99WO-US31274.

XX 08-MAR-1999; 99WO-US05028.

XX 21-APR-1999; 99US-0130232.

XX 26-APR-1999; 99US-0131022.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;  
 PI Wood WI;

XX WPI: 2000-638138/61.

XX N-PSDB; AAA75704.

XX A composition useful for treatment and diagnosis of a cardiovascular,  
 PT endothelial or angiogenic disorder, especially cancer, comprises (an  
 PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 PT PRO1330 or PRO1449 polypeptide -

XX Claim 67; Fig 14; 152pp; English.

XX The present sequence represents PRO1449, a human notch 4 homologue.  
 CC The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,  
 CC PRO1330 and PRO1449 polypeptides. The polypeptides promoter or  
 CC inhibit angiogenesis and cardiovascularisation in mammals. The  
 CC polypeptides are used for the treatment and diagnosis of a  
 CC cardiovascular, endothelial or angiogenic disorder, especially  
 CC cancer. Disorders that can be diagnosed, treated or prevented by  
 CC the polypeptides of the invention include trauma such as wounds,  
 CC arteriosclerosis, and cardiac hypertrophy.

XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQVYQFLLTCDGHR 60

Db 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQVYQFLLTCDGHR 60

QY 61 ACSTYRTIYRTAYRRSPGLAPARYACCPGWKRTSGLPAGCGAAICQPPCRNGGSCVQP 120

Db 61 ACSTYRTIYRTAYRRSPGLAPARYACCPGWKRTSGLPAGCGAAICQPPCRNGGSCVQP 120

QY 121 GRRCPCAGWRGDTQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPVK 180

Db 121 GRRCPCAGWRGDTQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPVK 180

QY 181 GPPRVAPNPTGVDKAMKEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

Db 181 GPPRVAPNPTGVDKAMKEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQQLGRIDSLSQISFLEQLGSCCKXDS 273



FT Modified-site /note= "Potential phosphorylation site"  
FT 205 /note= "Potential phosphorylation site"  
FT Modified-site 252 /note= "Potential phosphorylation site"  
FT 258 /note= "Potential phosphorylation site"  
FT Modified-site 268 /note= "Potential phosphorylation site"  
FT 273 /note= "Potential phosphorylation site"  
FT 273 /note= "Potential phosphorylation site"  
XX WO200034477-A2.  
XX 15-JUN-2000.  
XX 10-DEC-1999; 99WO-US30408.  
XX 11-DEC-1998; 98US-0210083.  
PR 11-DEC-1998; 98US-9123456.  
PR 09-FEB-1999; 99US-0119365.  
PR 16-MAR-1999; 99US-0124687.  
XX (INCYTE) INCYTE PHARM INC.  
XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;  
PI Lu DAM, Azimzai Y;  
PI WPI; 2000-423423/36.  
DR N-PSDB; AAA47417.  
XX New human neuron-associated proteins and polynucleotides encoding them,  
PT useful for diagnosis, treatment and prevention of cell proliferative  
PT disorders including cancer, neuronal and neurological disorders  
XX Claim 1; Page 97; 145pp; English.  
XX Human neuron-associated proteins (NEUAP) can be used for for  
CC treating or preventing a disorder associated with decreased  
CC expression or activity of NEUAP. Antagonists of NEUAP are useful for  
CC treating or preventing disorder associated with increased expression  
CC or activity of NEUAP. NEUAP or their fragments or derivatives are  
CC useful for treating neurological disorder such as epilepsy, ischemic  
CC cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's  
CC disease, Pick's disease, Huntington's disease, dementia and  
CC Parkinson's disease. NEUAPs are also useful for treating other  
CC demyelinating diseases, bacterial and viral meningitis, prion  
CC diseases including Kuru, Creutzfeldt-Jakob disease, nutritional and  
CC metabolic diseases of the nervous system, neurofibromatosis, other  
CC developmental disorders of the central nervous system, cerebral  
CC palsy, neuroskeletal disorders, autonomic nervous system disorders,  
CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and  
CC other neuromuscular disorders, peripheral nervous system disorders,  
CC inherited, metabolic, endocrine, and toxic myopathies, mental  
CC disorders including mood, anxiety and schizophrenic disorders, a cell  
CC proliferative disorder such as actinic keratosis, arteriosclerosis,  
CC atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective  
CC tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal  
CC haemoglobinuria, cancers of the adrenal gland, bladder, bone,  
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory  
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's  
CC disease, adult respiratory distress syndrome, allergies, ankylosing  
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,  
CC complications of cancer, hemodialysis, and extracorporeal circulation,  
CC viral, bacterial, fungal parasitic, protozoal, and helminthic  
CC infections, and trauma. This protein was given the Incyte ID no.  
CC 829443CD1.  
XX Sequence 273 AA;  
XX Query Match 100.0%; Score 1505; DB 21; Length 273;  
XX Best Local Similarity 100.0%; Pred. No. 1e-94;  
XX Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGTEHAYRPRRVCARVRAHGDVSESFYQRYVQPLTTCDGHR 60  
DB 1 MRGSEVLLMVLAVGTEHAYRPRRVCARVRAHGDVSESFYQRYVQPLTTCDGHR 60  
QY 61 ACSTYRTIYRTYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
DB 61 ACSTYRTIYRTYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
QY 121 GRCRCFAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCOCWEGHSLSDAGTLCVPKG 180  
DB 121 GRCRCFAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCOCWEGHSLSDAGTLCVPKG 180  
QY 181 GPRVAPNPTGVDSSAMKEEVQRLQSRVDLLEKLOLVLAHLPLSLASQALEHGLPDPGSL 240  
DB 181 GPRVAPNPTGVDSSAMKEEVQRLQSRVDLLEKLOLVLAHLPLSLASQALEHGLPDPGSL 240  
QY 241 VHSFQQLGRIDSLSEIOISFLEELGSCCKKDS 273  
DB 241 VHSFQQLGRIDSLSEIOISFLEELGSCCKKDS 273  
RESULT 7  
ID AAM23991 standard; Protein; 273 AA.  
XX AAM23991;  
XX 12-OCT-2001 (first entry)  
XX Human EST encoded protein SEQ ID NO: 1516.  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
XX diagnostic; forensic test; gene mapping; genetic disorder;  
XX biodiversity; gene therapy; nutrition.  
XX Homo sapiens.  
XX WO200154477-A2  
XX 02-AUG-2001  
XX 25-JAN-2001; 2001WO-US02687.  
XX 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX (HYSB-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
XX Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI; 2001-476164/51.  
XX N-PSDB; AAH98650.  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use -  
XX Claim 20; Page 1046-1047; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
XX proteins from a variety of organisms, including human, dog, cat, horse,  
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)  
XX from the organism of interest. They can be used in diagnostics,  
XX forensics, gene mapping, identification of mutations, to assess  
XX biodiversity and for nutritional purposes. The present sequence is a  
XX protein of the invention.  
XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 22; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 CC 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 181 GPRVAPNPFTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALBHGHPDPS 240  
 CC 181 GPRVAPNPFTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALBHGHPDPS 240  
 CC 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273  
 CC 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273

RESULT 8  
 AAB61609  
 ID AAB61609 standard; Protein; 273 AA.  
 XX AAB61609;  
 XX 05-APR-2001 (first entry)  
 XX Human protein HP03375.  
 DE Human protein HP03375.  
 KW Human; hydrophobic domain; immune deficiency; autoimmune disorder;  
 KW allergy; tissue growth; regeneration; wound healing; burn; tumour;  
 KW periodontal disease; thrombolytic condition; haemostatic condition;  
 KW infection.  
 OS Homo sapiens.  
 XX MO200102563-A2.  
 XX 11-JAN-2001.  
 XX 16-JUN-2000; 2000MO-JP03943.  
 XX 02-JUL-1999; 99UP-0188835.  
 XX (SAGA) SAGAMI CHEM RES CENT  
 XX (PROT-) PROTEGENE INC.  
 XX Kato S, Kimura T;  
 XX MPI; 2001-071581/08.  
 XX N-PSDB; AAF28680, AAF28690.  
 XX New human proteins with hydrophobic domains, useful for the treatment  
 XX of immune disorders, tumors, allergic conditions, thrombosis and  
 XX microbial infection -  
 XX Claim 1; Pages 97-98; 153p; English.  
 CC The present invention relates to human proteins (AAB61608-AAB61617) and  
 CC their coding sequences (AAF28679-AAF28698). The proteins of the present  
 CC invention have hydrophobic domains and can be used for the treatment of  
 CC various immune deficiencies and disorders, such as severe combined  
 CC immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis,  
 CC autoimmune pulmonary inflammation, graft-versus-host disease and  
 CC Guillain-Barre syndrome. The proteins may also be useful in the treatment  
 CC of allergic reactions and conditions, such as asthma and in regulation of

CC haematopoiesis or lymphoid cell deficiencies. The proteins may also have  
 CC utility in compositions used for bone, cartilage, tendon and/or nerve  
 CC tissue growth or regeneration as well as wound healing and in the  
 CC treatment of burns. The proteins may be used in the treatment of  
 CC periodontal disease and in other tooth repair processes. Other uses  
 CC include treatment of thrombolytic and haemostatic conditions, treatment  
 CC or prevention of tumours and inhibiting infection by bacteria, viruses,  
 CC fungi and other parasites.  
 CC Sequence 273 AA;  
 XX

Query Match 100.0%; Score 1505; DB 22; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 1 MRSGEVLMMVLVAVGTEHAHPRRCVCAVRAHGDVPSSEFVQRYVQPLTTCDGHR 60  
 CC 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 CC 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 CC 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 121 GRRCPCPAGMRGDTQSDVDECSARRGCCPQRCVNTAGSYWCQCEHSHLSADGTLCPV 180  
 CC 181 GPRVAPNPFTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALBHGHPDPS 240  
 CC 181 GPRVAPNPFTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALBHGHPDPS 240  
 CC 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273  
 CC 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273

RESULT 9  
 AAY41769  
 ID AAY41769 standard; Protein; 273 AA.  
 XX AAY41769;  
 XX 07-DEC-1999 (first entry)  
 XX Human PRO213-1 protein sequence.  
 DE Human PRO213-1 protein sequence.  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 OS Homo sapiens.  
 XX MO9946281-A2.  
 XX 16-SEP-1999.  
 XX 08-MAR-1999; 99MO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 XX 11-MAR-1998; 98US-0077632.  
 XX 11-MAR-1998; 98US-0077641.  
 XX 11-MAR-1998; 98US-0077649.  
 XX 12-MAR-1998; 98US-0077791.  
 XX 13-MAR-1998; 98US-0078004.  
 XX 17-MAR-1998; 98US-0040220.  
 XX 20-MAR-1998; 98US-0078886.  
 XX 20-MAR-1998; 98US-0078910.  
 XX 20-MAR-1998; 98US-0078936.  
 XX 20-MAR-1998; 98US-0078939.  
 XX 25-MAR-1998; 98US-0079294.  
 XX 26-MAR-1998; 98US-0079656.  
 XX 27-MAR-1998; 98US-0079663.  
 XX 27-MAR-1998; 98US-0079664.

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PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.

XX (GETH ) GENENTECH INC.
PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI: 1999-551358/46.
XX N-PSDB; AAZ34311.
DR
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX Claim 12; Fig 213; 530pp; English.
PS
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAZ41685 to AAZ41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 273 AA;
Query Match 99.9%; Score 1504; DB 20; Length 273;
Best Local Similarity 99.6%; Pred. No. 1.2e-94;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSQEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYVQPLTTCGHR 60
Db 1 MRGSQEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYVQPLTTCGHR 60
QY 61 ACSTYRTIYRTAYRSPGLAPAPRYACPGWKRTSGLPAGCAICOPPCRNNGSCVQP 120
Db 61 ACSTYRTIYRTAYRSPGLAPAPRYACPGWKRTSGLPAGCAICOPPCRNNGSCVQP 120
QY 121 GRCRCPAGWRGDTCSQDVDECSARRGGCPQRCVNTAGSYWCQCEGHSLSDGTLCPVK 180
Db 121 GRCRCPAGWRGDTCSQDVDECSARRGGCPQRCVNTAGSYWCQCEGHSLSDGTLCPVK 180
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSIL 240
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSIL 240
QY 241 VHSFQOLGRIDSLSBQISFLEELGSCSKKDS 273
Db 241 VHSFQOLGRIDSLSBQISFLEELGSCSKKDS 273

RESULT 10
AAZ41770
ID AAZ41770 standard; Protein; 273 AA.
XX
XX AAZ41770;
XX
XX 07-DEC-1999 (first entry)
XX
XX Human PRO1330 protein sequence.
DE
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
XX Homo sapiens.
OS
XX WO9946281-A2.
PN
XX 16-SEP-1999.
PD
XX
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PF 08-MAR-1999; 99WO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077649.  
 PR 12-MAR-1998; 98US-0077791.  
 PR 13-MAR-1998; 98US-0078004.  
 PR 17-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 25-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079294.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082569.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083332.  
 PR 29-APR-1998; 98US-0083392.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 30-APR-1998; 98US-0083559.  
 PR 05-MAY-1998; 98US-0083742.  
 PR 06-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084411.  
 PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084627.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.

PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085689.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 PI WPI; 1999-551358/46.  
 DR N-PSDB; AA234312.  
 XX  
 PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders -  
 XX  
 PS Claim 12; Fig 215; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA233891 to  
 CC AA23438 and AA24685 to AA24774 represent polynucleotides and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 20; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVILMMVLVAVGTEHAYRGRVCAVRAHGDVSEFVQRYOPLTTCDGHR 60  
 DB 1 MRGSEVILMMVLVAVGTEHAYRGRVCAVRAHGDVSEFVQRYOPLTTCDGHR 60  
 QY 61 ACSTYRTTYTAYRSPGLAPAPRYACCPGKRTSGLPACGAATCPGRNGSCVOP 120  
 DB 61 ACSTYRTTYTAYRSPGLAPAPRYACCPGKRTSGLPACGAATCPGRNGSCVOP 120  
 QY 121 GRCPAGMRGDTCCSDVDEGARRGCGPCPCNTAGSYWCQCHGSLSDGTLCPK 180  
 DB 121 GRCPAGMRGDTCCSDVDEGARRGCGPCPCNTAGSYWCQCHGSLSDGTLCPK 180  
 QY 181 GPRVAPNPTGVDSAMKEVORLQSRVDLLEBKLTQVLAPHSIASQALEGLDPPSLL 240  
 DB 181 GPRVAPNPTGVDSAMKEVORLQSRVDLLEBKLTQVLAPHSIASQALEGLDPPSLL 240  
 QY 241 VHSFOQLGRIDLSLOISLEBOLGSCCKKDS 273  
 DB 241 VHSFOQLGRIDLSLOISLEBOLGSCCKKDS 273  
 RESULT 11  
 AAB44325  
 ID AAB44325 standard; Protein; 273 AA.





PT cellular activities -  
 XX  
 PS Claim 12; Fig 215; 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

SO Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLVAVGTEHAHVRGRVCAVRAHGDVSESVFQRYOYQFLTTCDGHR 60  
 DB 1 MRGSEVLLMVLVAVGTEHAHVRGRVCAVRAHGDVSESVFQRYOYQFLTTCDGHR 60  
 QY 61 ACSTYRTIYRTAHRSPGLAPRPRACCPGKRTSGLPAGCAAIQCPPCRNCGSCVQP 120  
 DB 61 ACSTYRTIYRTAHRSPGLAPRPRACCPGKRTSGLPAGCAAIQCPPCRNCGSCVQP 120  
 QY 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180  
 DB 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180  
 QY 181 GPPRYAPNPTGVDMSAKKEVQRLQSRVLLBEKQLVLAPLHSIASQALEKLPDPSSL 240  
 DB 181 GPPRYAPNPTGVDMSAKKEVQRLQSRVLLBEKQLVLAPLHSIASQALEKLPDPSSL 240  
 QY 241 VHSFOQLGRIDSLSEQISFLEFOLGSCCKKDS 273  
 DB 241 VHSFOQLGRIDSLSEQISFLEFOLGSCCKKDS 273

# RESULT 13

AAB18673  
 ID AAB18673 standard; Protein; 273 AA.

AC AAB18673;  
 AC XX

DT 22-JAN-2001 (first entry)

XX Amino acid sequence of a human a PRO213 polypeptide.

DE Growth arrest-specific gene 6 protein homologue; PRO320; PRO938; PRO1031;  
 KW PRO296; PRO213; PRO1449; angiogenesis; cardiovascularisation; PRO1330;  
 KW cardiovascular disorder; endothelial disorder; angiogenic disorder;  
 KW cancer; trauma; wound; atherosclerosis; cardiac hypertrophy.  
 XX  
 OS Homo sapiens.

XX Key  
 FT Peptide  
 FT Location/Qualifiers  
 FT 1..19  
 FT /note= "signal sequence"  
 FT Modified-site  
 FT 19..25  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 26..30  
 FT /note= "amidation site"  
 FT Modified-site  
 FT 78..84  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 93..97  
 FT /note= "CAMP- and GMP-dependent protein kinase  
 FT phosphorylation site"  
 FT Modified-site  
 FT 97..103

FT /note= "N-myristoylation site"  
 FT 100..106  
 FT /note= "N-myristoylation site"  
 FT 103..109  
 FT /note= "N-myristoylation site"  
 FT 123..135  
 FT /note= "EGF-like domain cysteine pattern signature"  
 FT 130..133  
 FT /note= "cell attachment sequence"  
 FT 152..164  
 FT /note= "aspartic acid and asparagine hydroxylation site"  
 FT 157..163  
 FT /note= "N-myristoylation site"  
 FT 191..197  
 FT /note= "N-myristoylation site"  
 FT 265..271  
 FT /note= "N-myristoylation site"  
 FT  
 XX  
 XX  
 PN WO200053752-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PD 30-DEC-1999; 99WO-US31274.  
 XX  
 PD 08-MAR-1999; 99WO-US05028.  
 XX  
 PR 21-APR-1999; 99US-0130232.  
 PR 26-APR-1999; 99US-0131022.  
 PR 28-APR-1999; 99US-0131445.  
 PR 02-DEC-1999; 99US-0134287.  
 PR 02-DEC-1999; 99US-0134287.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;  
 PI Wood WI;  
 PI WPI: 2000-638138/61.  
 DR N-PSDB; AAA75702.  
 DR

A composition useful for treatment and diagnosis of a cardiovascular,  
 endothelial or angiogenic disorder, especially cancer, comprises (an  
 agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 PRO1330 or PRO1449 polypeptide -  
 XX  
 XX  
 PS Claim 67; Fig 10; 152pp; English.

CC The present sequence represents PRO213, a human growth arrest-specific  
 CC gene 6 protein homologue. The specification describes PRO320, PRO938,  
 CC PRO1031, PRO296, PRO213, and PRO1449 polypeptides. The  
 CC polypeptides promoter or inhibit angiogenesis and cardiovascularisation  
 CC in mammals. The polypeptides are used for the treatment and diagnosis  
 CC of a cardiovascular, endothelial or angiogenic disorder, especially  
 CC cancer. Disorders that can be diagnosed, treated or prevented by  
 CC the polypeptides of the invention include trauma such as wounds,  
 CC atherosclerosis, and cardiac hypertrophy.

SO Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLVAVGTEHAHVRGRVCAVRAHGDVSESVFQRYOYQFLTTCDGHR 60  
 DB 1 MRGSEVLLMVLVAVGTEHAHVRGRVCAVRAHGDVSESVFQRYOYQFLTTCDGHR 60  
 QY 61 ACSTYRTIYRTAHRSPGLAPRPRACCPGKRTSGLPAGCAAIQCPPCRNCGSCVQP 120  
 DB 61 ACSTYRTIYRTAHRSPGLAPRPRACCPGKRTSGLPAGCAAIQCPPCRNCGSCVQP 120  
 QY 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180  
 DB 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180

Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;  
Wood WI;  
WPI: 2000-638138/61.  
N-PSDB; AAA75703.

A composition useful for treatment and diagnosis of a cardiovascular, endothelial or angiogenic disorder, especially cancer, comprises (an agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213, PRO1330 or PRO1449 polypeptide -

Claim 67; Fig 12; 152pp; English.

The present sequence represents PRO1330, a human notch 4 homologue. The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213, PRO1330 and PRO1449 polypeptides. The polypeptides promoter or inhibit angiogenesis and cardiovascularisation in mammals. The polypeptides are used for the treatment and diagnosis of a cardiovascular, endothelial or angiogenic disorder, especially cancer. Disorders that can be diagnosed, treated or prevented by the polypeptides of the invention include trauma such as wounds, CC arteriosclerosis, and cardiac hypertrophy.

Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred No. 1.2e-94;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGQEVLLMWLLVAVGGTEHAYRFRVCAVRAHGDVSEFVQVYQPLTTCDGHR 60  
Db 1 MRGQEVLLMWLLVAVGGTEHAYRFRVCAVRAHGDVSEFVQVYQPLTTCDGHR 60  
QY 61 ACSTYRTIYRTARRSPCLAPAPRYACCPGWKRTSLGACGAALCQPPCRNGSCVQP 120  
Db 61 ACSTYRTIYRTARRSPCLAPAPRYACCPGWKRTSLGACGAALCQPPCRNGSCVQP 120  
QY 121 GRCCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180  
Db 121 GRCCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180  
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
QY 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273  
Db 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273

RESULT 15  
AAB24042  
ID AAB24042 standard; Protein; 273 AA.  
XX  
AC AAB24042;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Human PRO213 protein sequence SEQ ID NO:4.  
XX  
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
KW tumorigenesis; detection; neoplastic cell growth; proliferation;  
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;  
KW immunological disorder.  
OS Homo sapiens.  
XX  
PN WO200053754-A1.  
XX  
PD 14-SEP-2000.  
XX  
PF 06-JAN-2000; 2000WO-US00277.  
XX

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
QY 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273  
Db 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273

RESULT 14

AAB18674  
ID AAB18674 standard; Protein; 273 AA.

XX  
AC AAB18674;

DT 22-JAN-2001 (first entry)

XX Amino acid sequence of a human PRO1330 polypeptide.

DE Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO1449;  
XX angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;  
KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
KW arteriosclerosis; cardiac hypertrophy.

XX Homo sapiens.

XX Location/Qualifiers

Key 1..19  
FT Peptide /note= "signal sequence"  
FT Modified-site 19..25 /note= "N-myristoylation site"  
FT Modified-site 26..30 /note= "amidation site"  
FT Modified-site 78..84 /note= "N-myristoylation site"  
FT Modified-site 93..97 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT Modified-site 97..103 /note= "N-myristoylation site"  
FT Modified-site 100..106 /note= "N-myristoylation site"  
FT Modified-site 103..109 /note= "N-myristoylation site"  
FT Region 123..135 /note= "EGF-like domain cysteine pattern signature"  
FT Region 130..133 /note= "cell attachment sequence"  
FT Modified-site 152..164 /note= "aspartic acid and asparagine hydroxylation site"  
FT Modified-site 157..163 /note= "N-myristoylation site"  
FT Modified-site 191..197 /note= "N-myristoylation site"  
FT Modified-site 265..271 /note= "N-myristoylation site"

XX WO200053752-A2.

XX 14-SEP-2000.

XX 30-DEC-1999; 99WO-US31274.

XX 08-MAR-1999; 99WO-US05028.

XX 21-APR-1999; 99US-0130232.

XX 26-APR-1999; 99US-0131022.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 29-MAR-1999; 99US-0126773.  
PR 21-APR-1999; 99US-0130232.  
PR 28-APR-1999; 99US-0131445.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 30-DEC-1999; 99WO-US28564.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.

XX (GETH ) GENENTECH INC.

XX Baker KP, Desauvage FT, Goddard A, Gurney AL, Klein RD, Roy MA;  
PI Wood WI;

XX WPI; 2000-572269/53.  
DR N-PSDB; AAC58226.

XX New isolated antibody for use in compositions and methods for the  
PT diagnosis and treatment of neoplastic cell growth and proliferation in  
PT mammals, including humans, and in monitoring tumor treatment -  
XX  
XX Claim 61; Fig 4; 195pp; English.

XX The present invention describes an isolated antibody (Ab) that binds to  
CC one of the human proteins (P) designated PRO213, PRO1310, PRO1449,  
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO364, PRO618,  
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions  
CC and methods for the diagnosis and treatment of neoplastic cell growth  
CC and proliferation in mammals, including humans. Genes and polypeptides  
CC encoded by them, that are amplified in the genome of a tumour cell, can  
CC be identified and are useful targets for the treatment and prevention of  
CC certain cancers and may be used to monitor tumour treatment. Compounds  
CC that inhibit the expression or activity of the identified polypeptides  
CC can be identified and used as antagonists. Benign or malignant tumours,  
CC inflammatory disorders and immunological disorders can be treated.  
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

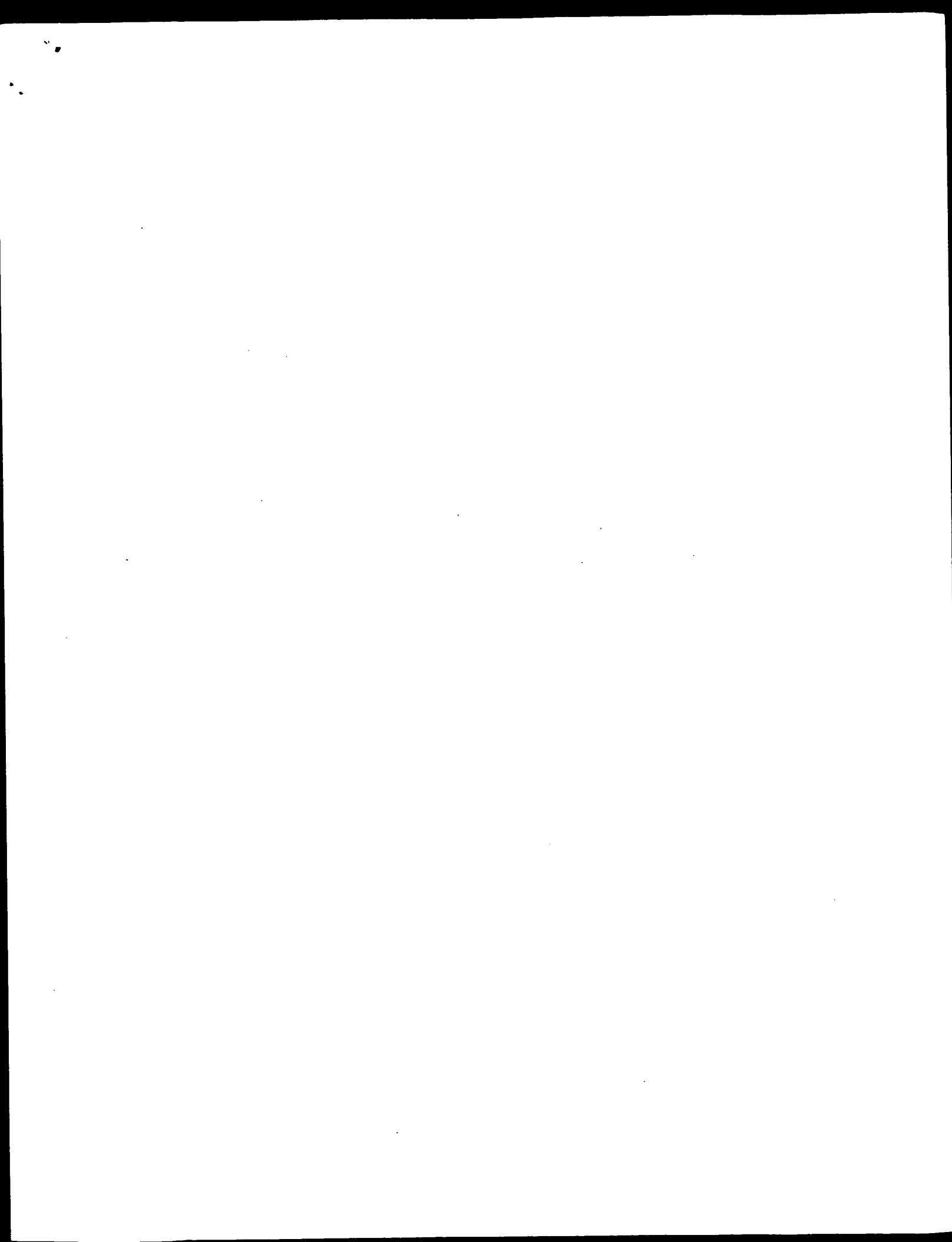
XX SQ Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;

Best Local Similarity 99.6%; Pred. No. 1.2e-94;

Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMLVLAAGTEHAYPGRRCVCAVRAHGDVPSFVQRYVQPLTTCDDHR 60  
DB 1 MRGSOEVLMLVLAAGTEHAYPGRRCVCAVRAHGDVPSFVQRYVQPLTTCDDHR 60  
QY 61 ACSTYRTIYTAIRRSBGLAPAPRRYACCPGWRKTSGLPGACGAACIQPPCRNGSSCVQ 120  
DB 61 ACSTYRTIYTAIRRSBGLAPAPRRYACCPGWRKTSGLPGACGAACIQPPCRNGSSCVQ 120  
QY 121 GRRCPCAGMGDTCCSDVDECSARRGGCPQRCVNTAGSTWCOCMEGHSLSADGTLCPKG 180  
DB 121 GRRCPCAGMGDTCCSDVDECSARRGGCPQRCVNTAGSTWCOCMEGHSLSADGTLCPKG 180  
QY 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLEERKQLVLAFLHSLASQALBHGGLPDPSGL 240  
DB 181 GPPRVAPNPTGVDSAMKEEVORLQSRVDLEERKQLVLAFLHSLASQALBHGGLPDPSGL 240  
QY 241 VHSFOQLGRIDSLEQISFLERQLSCKKDS 273  
DB 241 VHSFOQLGRIDSLEQISFLERQLSCKKDS 273



GenCore version 5.1.3  
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OM protein - protein search, using SW model

Run on: December 17, 2002, 10:00:46 ; Search time 13.4687 Seconds

(without alignments)  
596.380 Million cell updates/sec

Title: US-09-852-472-2

Perfect score: 1505  
Sequence: 1 MRSGQEVLLMMLVLAAGT.....SEQISFLEQLGSCCKD 273

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA.\*  
1: /cgnt\_6/ptodata/1/1aa/5A.COMB.pdp.\*  
2: /cgnt\_6/ptodata/1/1aa/5B.COMB.pdp.\*  
3: /cgnt\_6/ptodata/1/1aa/6A.COMB.pdp.\*  
4: /cgnt\_6/ptodata/1/1aa/6B.COMB.pdp.\*  
5: /cgnt\_6/ptodata/1/1aa/PTUS.COMB.pdp.\*  
6: /cgnt\_6/ptodata/1/1aa/backfile1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Length | DB ID | Description                         |
|------------|-------|--------------|-------|-------------------------------------|
| 1          | 1181  | 78.5         | 4     | US-09-724-864-52 Sequence 52, Appl  |
| 2          | 255.5 | 17.0         | 4     | US-09-249-697A-6 Sequence 6, Appl   |
| 3          | 255.5 | 17.0         | 4     | US-09-363-316B-6 Sequence 6, Appl   |
| 4          | 252.5 | 16.8         | 4     | US-09-249-697A-19 Sequence 19, Appl |
| 5          | 252.5 | 16.8         | 4     | US-09-363-316B-24 Sequence 24, Appl |
| 6          | 217.5 | 14.5         | 4     | US-09-249-697A-18 Sequence 18, Appl |
| 7          | 217.5 | 14.5         | 4     | US-09-363-316B-4 Sequence 4, Appl   |
| 8          | 217.5 | 14.4         | 4     | US-09-249-697A-3 Sequence 3, Appl   |
| 9          | 216.5 | 14.4         | 4     | US-09-363-316B-3 Sequence 3, Appl   |
| 10         | 216.5 | 14.0         | 4     | US-09-467-997-1 Sequence 1, Appl    |
| 11         | 189   | 12.6         | 4     | US-08-282-141-2 Sequence 2, Appl    |
| 12         | 189   | 12.6         | 4     | US-08-435-434-2 Sequence 2, Appl    |
| 13         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 14         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 15         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 16         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 17         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 18         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 19         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 20         | 189   | 12.6         | 4     | US-08-438-864-2 Sequence 2, Appl    |
| 21         | 184   | 12.2         | 4     | US-08-435-434-1 Sequence 1, Appl    |
| 22         | 184   | 12.2         | 4     | US-08-438-864-1 Sequence 1, Appl    |
| 23         | 184   | 12.2         | 4     | US-08-438-864-1 Sequence 1, Appl    |
| 24         | 184   | 12.2         | 4     | US-08-438-864-1 Sequence 1, Appl    |
| 25         | 184   | 12.2         | 4     | US-08-438-864-1 Sequence 1, Appl    |
| 26         | 184   | 12.2         | 4     | US-08-438-864-1 Sequence 1, Appl    |
| 27         | 184   | 12.2         | 4     | US-08-628-747-1 Sequence 1, Appl    |

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|----|-------|------|------|---|-------------------|-------------------|
| 28 | 184   | 12.2 | 673  | 4 | US-08-402-253-1   | Sequence 1, Appl  |
| 29 | 184   | 12.2 | 673  | 4 | US-08-443-868B-1  | Sequence 1, Appl  |
| 30 | 183   | 12.2 | 810  | 3 | US-08-820-170A-34 | Sequence 34, Appl |
| 31 | 183   | 12.2 | 810  | 3 | US-09-055-699-34  | Sequence 34, Appl |
| 32 | 183   | 12.2 | 810  | 3 | US-09-273-565-34  | Sequence 34, Appl |
| 33 | 183   | 12.2 | 810  | 4 | US-09-565-538-34  | Sequence 34, Appl |
| 34 | 183   | 12.2 | 810  | 4 | US-09-661-468-34  | Sequence 34, Appl |
| 35 | 181.5 | 12.1 | 816  | 2 | US-08-820-170A-37 | Sequence 37, Appl |
| 36 | 181.5 | 12.1 | 816  | 3 | US-09-055-699-37  | Sequence 37, Appl |
| 37 | 181.5 | 12.1 | 816  | 4 | US-09-273-565-37  | Sequence 37, Appl |
| 38 | 181.5 | 12.1 | 816  | 4 | US-09-565-538-37  | Sequence 37, Appl |
| 39 | 181.5 | 12.1 | 816  | 4 | US-09-661-468-37  | Sequence 37, Appl |
| 40 | 176   | 11.7 | 652  | 2 | US-08-751-305-2   | Sequence 37, Appl |
| 41 | 176   | 11.7 | 2703 | 1 | US-08-185-432-19  | Sequence 2, Appl  |
| 42 | 176   | 11.7 | 2703 | 4 | US-08-899-232-4   | Sequence 19, Appl |
| 43 | 173.5 | 11.5 | 1833 | 3 | US-08-479-722B-2  | Sequence 2, Appl  |
| 44 | 173.5 | 11.5 | 1833 | 5 | PCT-US95-02251-18 | Sequence 4, Appl  |
| 45 | 169   | 11.2 | 830  | 3 | US-08-872-855-11  | Sequence 18, Appl |

## ALIGNMENTS

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RESULT 1
US-09-724-864-52
; Sequence 52, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: By the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-52

Query Match      78.5%; Score 1181; DB 4; Length 278;
Best Local Similarity 78.1%; Pred. No. 8.1e-87;
Matches 214; Conservative 18; Mismatches 40; Indels 2; Gaps 2;

QY 1 MRSGQEVLLMMLVLAAGT-TEHAYRPGRRVCAVAHAGDPVSEFVORVYQFLTTCDGH 59
DB 4 MMGSGELVLAAMVLAADDTTHVYRPSRVCTVIGISGSISETIVQRYOYDPLTCDGH 63
QY 60 RACSTYRTTYRATYRPSRGLAPARPRVACCPGKRTSGIPGACGAICOPPCRNKSGCVQ 119
DB 64 RACSTYRTTYRATYRPSRGLAPARPRVACCPGKRTSGIPGACGAICOPPCRNKSGCIR 123
QY 120 PGRCPGAPWRDGTQSDVDECSARGGCPQRCVNTATSYCCQCEHGSLSADGTLCPK 179
DB 124 PGRCPGAPWRDGTQSDVDECSARGGCPQRCVNTATSYCCQCEHGSLSADGTLCPK 183
QY 180 GGPFRVAPNPT-GVDSAMKEEYORLQSHVLDLEKQLQVLAFLSHLSAQLHGLPDPGS 238
DB 184 EGPSPVAPNPTAGVDSAMKEEYORLQSHVLDLEKQLQVLAFLSHLSAQLHGLPDPGS 243
QY 233 LLVHFFQGLRDLISLSEQISFLEQLGSCCKD 272
DB 244 LLVHFFQGLRDLISLSEQISFLEQLGSCCKD 277

RESULT 2
US-09-249-697A-6
; Sequence 6, Application US/09249697A
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      QY      91  GMRKTSGLPGACGAALICPPCRNNGSCVQPPRCRCPPAGMRGDTTCQSDVDECSARAGGCPQ 150
      Db      1  GMRKRS--KQVC-EATCEBCK-FCECVGPVKRCFPFGYTKTCSQDVNCGMKRPPCQH 56
      QY      151 RCNVTAGSIWCCQEGSHLSADGTLCV-----PKGPP-----RVA 186
      Db      57 RCNVTAGSIWCCQEGSHLSADGTLCV-----PKGPP-----RVA 115

      QY      187 PN 188
      Db      116 PN 117

      RESULT 8
      US-09-363-316B-4
      ; Sequence 4, Application US/09363316B
      ; Patent No. 6392019
      ; GENERAL INFORMATION:
      ; APPLICANT: Ford, John
      ; APPLICANT: Yeung, George
      ; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
      ; FILE REFERENCE: 28110/35852
      ; CURRENT APPLICATION NUMBER: US/09/363,316B
      ; PRIOR FILING DATE: 1999-07-28
      ; PRIOR APPLICATION NUMBER: US 09/249,697
      ; PRIOR FILING DATE: 1999-02-12
      ; PRIOR APPLICATION NUMBER: US 08/968,800
      ; PRIOR FILING DATE: 1997-11-22
      ; NUMBER OF SEQ ID NOS: 24
      ; SOFTWARE: FastSeq for Windows Version 3.0
      ; SEQ ID NO 4
      ; LENGTH: 537
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; FEATURE:
      ; NAME/KEY: misc feature
      ; LOCATION: (503)
      ; OTHER INFORMATION: Xaa = any amino acid
      US-09-363-316B-4

      Query Match      14.5%; Score 217.5; DB 4; Length 537;
      Best Local Similarity 40.2%; Pred. No. 9.6e-10;
      Matches 49; Conservative 9; Mismatches 35; Indels 29; Gaps 6

      QY      91  GMRKTSGLPGACGAALICPPCRNNGSCVQPPRCRCPPAGMRGDTTCQSDVDECSARAGGCPQ 150
      Db      1  GMRKRS--KQVC-EATCEBCK-FCECVGPVKRCFPFGYTKTCSQDVNCGMKRPPCQH 56
      QY      151 RCNVTAGSIWCCQEGSHLSADGTLCV-----PKGPP-----RVA 186
      Db      57 RCNVTAGSIWCCQEGSHLSADGTLCV-----PKGPP-----RVA 115

      QY      187 PN 188
      Db      116 PN 117

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## RESULT 9

US-09-249-697A-3

; Sequence 3, Application US/09249697A

; Patent No. 6392018

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL

; FILE REFERENCE: LIVER SPLEEN

; CURRENT APPLICATION NUMBER: US/09/249,697A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 08/968,800

; PRIOR FILING DATE: 1997-11-22

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-249-697A-3

## Query Match

Best Local Similarity 14.4%; Score 216.5; DB 4; Length 100;

Matches 43; Conservative 7; Mismatches 32; Indels 5; Gaps 4;

QY 91

GWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTQSDVDECSARRGGCPQ 150

DB 1 GWRNRS--KGVC-EATCEPGCK-FGECVGNKCRCFPGYTGKTCSDQVNECGMKPRPCQH 56

QY 151

RCVNTAGSYWCQCEGHSLSDGTLVCV 177

DB 57 RCVNTHGSKYKFCCLSGHMLMPDAT-CV 82

## RESULT 10

US-09-363-316B-3

; Sequence 3, Application US/09363316B

; Patent No. 6392019

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS

; FILE REFERENCE: 28110/35852

; CURRENT APPLICATION NUMBER: US/09/363,316B

; CURRENT FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: US 09/249,697

; PRIOR FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 08/968,800

; PRIOR FILING DATE: 1997-11-22

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-363-316B-3

## Query Match

Best Local Similarity 14.4%; Score 216.5; DB 4; Length 100;

Matches 43; Conservative 7; Mismatches 32; Indels 5; Gaps 4;

QY 91

GWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTQSDVDECSARRGGCPQ 150

DB 1 GWRNRS--KGVC-EATCEPGCK-FGECVGNKCRCFPGYTGKTCSDQVNECGMKPRPCQH 56

QY 151

RCVNTAGSYWCQCEGHSLSDGTLVCV 177

DB 57 RCVNTHGSKYKFCCLSGHMLMPDAT-CV 82

## RESULT 11

US-09-467-997-1

; Sequence 1, Application US/09467997

; Patent No. 6379925

; GENERAL INFORMATION:

; APPLICANT: Kitajewski, Jan

; APPLICANT: Uyttendaele, Hendrik

; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION

; FILE REFERENCE: 53863-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/467,997

; CURRENT FILING DATE: 1999-12-20

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1964

; TYPE: PRT

; ORGANISM: mouse

US-09-467-997-1

## Query Match

Best Local Similarity 13.0%; Score 196; DB 4; Length 1964;

Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

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DB 134 ASGRQCCEPGEWTGEQQLRDFCSA-----NPCANGGVCLATYFQIQRCRPPGEGHTCE 189

QY 136 SDVDECSARRGGCPQ--RCVNTAGSYWCQ---WEHSLSDGTLVCP---KGGPRVA 186

DB 190 RDINECFLEPGPCPGTSGHNTLGSYQCLFVQGGPQCKLRKKGACPGSCINGGTCLV 249

QY 187 PNP-----TGVDSAMKEE 199

DB 250 PEGHSTFHLCLCPPGFTGLDCEMNP 275

## RESULT 12

US-08-282-141-2

; Sequence 2, Application US/08282141

; Patent No. 5538861

; GENERAL INFORMATION:

; APPLICANT: Schneider, Claudio

; APPLICANT: Varnum, Brian

; APPLICANT: Avanzi, Giancarlo

; APPLICANT: Brancolini, Claudio

; APPLICANT: Manfioletti, Guidalberto

; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: United States

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/282,141

; FILING DATE:

; CLASSIFICATION: 435

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 678 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-282-141-2



Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPELTTCDDH-----RACSTYRTYRTAYRSPGLAPRPYACC-----PGWK 93  
DB 47 RRAQVFEAKQGHLEBCEVELCS--REARVEFENDPETDYFPRYLDCTINKYSPYT 104  
QY 94 RTSG-----LPACGAAICQPPC-RNGGSCVOP--GR--CRCPAGWBDTCOSDVEDC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNPCRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160  
QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGSFHCSHGFEISDGRTC 195

## RESULT 13

US-08-435-434-2  
Sequence 2, Application US/08435434  
Patent No. 5714385  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,434  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-434-2

Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPELTTCDDH-----RACSTYRTYRTAYRSPGLAPRPYACC-----PGWK 93  
DB 47 RRAQVFEAKQGHLEBCEVELCS--REARVEFENDPETDYFPRYLDCTINKYSPYT 104  
QY 94 RTSG-----LPACGAAICQPPC-RNGGSCVOP--GR--CRCPAGWBDTCOSDVEDC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNPCRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160

QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGSFHCSHGFEISDGRTC 195

## RESULT 14

US-08-435-436-2  
Sequence 2, Application US/08435436  
Patent No. 5721139  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,436  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-436-2

Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPELTTCDDH-----RACSTYRTYRTAYRSPGLAPRPYACC-----PGWK 93  
DB 47 RRAQVFEAKQGHLEBCEVELCS--REARVEFENDPETDYFPRYLDCTINKYSPYT 104  
QY 94 RTSG-----LPACGAAICQPPC-RNGGSCVOP--GR--CRCPAGWBDTCOSDVEDC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNPCRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160  
QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGSFHCSHGFEISDGRTC 195

## RESULT 15

US-08-438-863-2  
Sequence 2, Application US/08438863  
Patent No. 5849585  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Ronghao Li



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 10:03:07 ; Search time 8.80645 Seconds  
(without alignments)  
516.533 Million cell updates/sec

Title: US-09-852-472-2

Perfect score: 1505  
Sequence: 1 MNGSQEVLMLVLAAGT.....SEQISFLEQLGSCCKKDS 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 segs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/prodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
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13: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID                 | Description       |
|------------|--------|-------------|--------|--------------------|-------------------|
| 1          | 1505   | 100.0       | 273    | US-09-978-295A-510 | Sequence 510, App |
| 2          | 1505   | 100.0       | 273    | US-09-978-697-510  | Sequence 510, App |
| 3          | 1505   | 100.0       | 273    | US-09-978-192A-510 | Sequence 510, App |
| 4          | 1504   | 99.9        | 273    | US-09-978-295A-506 | Sequence 506, App |
| 5          | 1504   | 99.9        | 273    | US-09-978-295A-508 | Sequence 508, App |
| 6          | 1504   | 99.9        | 273    | US-09-978-697-506  | Sequence 506, App |
| 7          | 1504   | 99.9        | 273    | US-09-978-697-508  | Sequence 508, App |
| 8          | 1504   | 99.9        | 273    | US-09-978-192A-506 | Sequence 506, App |
| 9          | 1504   | 99.9        | 273    | US-09-978-192A-508 | Sequence 508, App |
| 10         | 1504   | 99.9        | 273    | US-09-978-264-10   | Sequence 10, App  |
| 11         | 1392   | 92.5        | 251    | US-09-790-264-12   | Sequence 12, App  |
| 12         | 1340.5 | 89.1        | 295    | US-09-978-295A-2   | Sequence 2, App   |
| 13         | 1340.5 | 89.1        | 295    | US-09-978-697-2    | Sequence 2, App   |
| 14         | 1340.5 | 89.1        | 295    | US-09-978-192A-2   | Sequence 2, App   |
| 15         | 1181   | 78.5        | 275    | US-09-790-264-15   | Sequence 15, App  |
| 16         | 945.5  | 62.8        | 287    | US-09-764-898-218  | Sequence 218, App |
| 17         | 945.5  | 62.8        | 288    | US-09-764-853-841  | Sequence 841, App |
| 18         | 945.5  | 62.8        | 288    | US-09-764-898-290  | Sequence 290, App |
| 19         | 945.5  | 62.8        | 314    | US-09-764-853-670  | Sequence 670, App |

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|----|-------|------|------|----|--------------------|-------------------|
| 20 | 919.5 | 61.1 | 247  | 10 | US-09-790-264-20   | Sequence 20, App  |
| 21 | 255.5 | 17.0 | 553  | 9  | US-09-981-649A-6   | Sequence 6, App   |
| 22 | 252.5 | 16.8 | 338  | 9  | US-09-978-295A-119 | Sequence 119, App |
| 23 | 252.5 | 16.8 | 338  | 9  | US-09-978-697-119  | Sequence 119, App |
| 24 | 252.5 | 16.8 | 338  | 9  | US-09-978-192A-119 | Sequence 119, App |
| 25 | 252.5 | 16.8 | 553  | 10 | US-09-981-649A-24  | Sequence 24, App  |
| 26 | 252.5 | 16.8 | 554  | 10 | US-09-981-649A-32  | Sequence 32, App  |
| 27 | 250.5 | 16.6 | 554  | 10 | US-09-981-649A-30  | Sequence 30, App  |
| 28 | 250.5 | 16.6 | 559  | 9  | US-09-981-649A-28  | Sequence 28, App  |
| 29 | 223   | 14.8 | 509  | 10 | US-09-905-291A-315 | Sequence 315, App |
| 30 | 223   | 14.8 | 509  | 10 | US-09-909-320-315  | Sequence 315, App |
| 31 | 223   | 14.8 | 509  | 10 | US-09-909-088B-315 | Sequence 315, App |
| 32 | 223   | 14.8 | 509  | 12 | US-10-052-586-52   | Sequence 52, App  |
| 33 | 217.5 | 14.5 | 502  | 10 | US-09-981-649A-18  | Sequence 18, App  |
| 34 | 217.5 | 14.5 | 537  | 10 | US-09-981-649A-4   | Sequence 4, App   |
| 35 | 216.5 | 14.4 | 100  | 10 | US-09-981-649A-3   | Sequence 3, App   |
| 36 | 207   | 13.8 | 201  | 10 | US-09-764-853-797  | Sequence 797, App |
| 37 | 207   | 13.8 | 201  | 10 | US-09-764-898-270  | Sequence 270, App |
| 38 | 184   | 12.2 | 652  | 10 | US-09-789-919-96   | Sequence 96, App  |
| 39 | 183   | 12.2 | 810  | 10 | US-09-976-165-34   | Sequence 34, App  |
| 40 | 181.5 | 12.1 | 816  | 10 | US-09-976-165-37   | Sequence 37, App  |
| 41 | 173.5 | 11.5 | 1246 | 10 | US-09-919-497-85   | Sequence 85, App  |
| 42 | 172   | 11.4 | 534  | 10 | US-09-804-156-14   | Sequence 14, App  |
| 43 | 172   | 11.4 | 534  | 10 | US-09-946-633-6    | Sequence 6, App   |
| 44 | 169   | 11.2 | 1055 | 10 | US-09-855-722-2    | Sequence 2, App   |
| 45 | 166   | 11.0 | 1212 | 10 | US-09-855-722-3    | Sequence 3, App   |

## ALIGNMENTS

RESULT 1  
US-09-978-295A-510  
; Sequence 510, Application US/09978295A  
; Patent No. US20020156006A1  
GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Bostein, David  
; APPLICANT: Deamoysers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT FILING DATE: US/09/978, 295A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249

[illegible]

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.2e+100;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGEVLMMVLVAVGTEHAYRGRRCVCAVRAHGDVPSSEFVQRYQPTTCDGHR 60  
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QY 61 AGSTYRTYATVARSFGLAPARPRYACCPGMRKTSGLPGACGAICOPPCRRGSSCVQ 120  
DB 61 AGSTYRTYATVARSFGLAPARPRYACCPGMRKTSGLPGACGAICOPPCRRGSSCVQ 120  
QY 121 GRCRCPAWBGDTQSDVDDECSARRGCPQRCVNTAGSYWCQCEHSHLSADDTLCPK 180  
DB 121 GRCRCPAWBGDTQSDVDDECSARRGCPQRCVNTAGSYWCQCEHSHLSADDTLCPK 180  
QY 181 GPRVAVNPFGVDSAMKEEYQRLQSRVDLEEKQLVLAHSLASQALHGLPDPGSL 240  
DB 181 GPRVAVNPFGVDSAMKEEYQRLQSRVDLEEKQLVLAHSLASQALHGLPDPGSL 240  
QY 241 VHSFQQLGRIDSLEQISFLEQLGSCCKDS 273  
DB 241 VHSFQQLGRIDSLEQISFLEQLGSCCKDS 273

RESULT 2  
US-09-978-697-510  
Sequence 510, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guirney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/077791  
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; PRIOR FILING DATE: 1998-05-07

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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GRCRCPAGWRGDTQSDYDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVGK 180  
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QY 181 GPRVAPNPVTGVDKAMKEEVQRLQSRVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
DB 181 GPRVAPNPVTGVDKAMKEEVQRLQSRVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKXDS 273  
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## RESULT 3

US-09-978-192A-510  
; Sequence 510, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: Acids Encoding the Same  
CURRENT APPLICATION NUMBER: US/09/978,192A  
PRIOR FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639

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PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
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 PRIOR FILING DATE: 1998-05-07  
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 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 9; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 241 VHSFQQLGRIDSLSEQLSFLEEQLGSCCKKDS 273

RESULT 4  
 US-09-978-295A-506  
 Sequence 506 Application US/09378295A  
 Patent No. US2002015606A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Fertara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
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 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630FIC11  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

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 QY 241 VHSFOQLGRIDSLSQISFLBEQJGSCCKKDS 273  
 DB 241 VHSFOQLGRIDSLSQISFLBEQJGSCCKKDS 273

RESULT 5  
 US-09-978-295A-508  
 ; Sequence 508, Application US/09978295A  
 ; Patent No. US20020156006A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

us-09-852-472-2.rapb

Tue Dec 17 14:03:48 2002

APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
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 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630PIC11  
 CURRENT APPLICATION NUMBER: US/09/978,295A  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.98; Score 1504; DB 9; Length 273;  
Best Local Similarity 99.64; Pred. No. 1.5e-100;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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181 GPPVAPVPTGVSAMKEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPSSL 240  
181 GPPVAPVPTGVSAMKEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPSSL 240  
241 VHSFOUGRIDSLSEQISFLBEQJGSCCKDS 273  
VHSFOUGRIDSLSEQISFLBEQJGSCCKDS 273

Db 241 VHSFOUGRIDSLSEQISFLBEQJGSCCKDS 273

RESULT 6  
US-09-978-697-506  
Sequence 506, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630FIC27  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
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APPLICANT: Kuo, Sophia S.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
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PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797

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RESULT 8  
US-09-978-192A-506  
; Sequence 506, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630F1C9  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/918585  
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Query Match 99.9%; Score 1504; DB 9; Length 273;  
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Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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| 56 | PRIOR FILING DATE: 1998-05-07         |
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| 69 | PRIOR APPLICATION NUMBER: 60/085579   |
| 70 | PRIOR FILING DATE: 1998-05-15         |
| 71 | PRIOR APPLICATION NUMBER: 60/085580   |
| 72 | PRIOR FILING DATE: 1998-05-15         |
| 73 | PRIOR APPLICATION NUMBER: 60/085573   |

Tue Dec 17 14:03:48 2002

; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
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Query Match 99.9%; Score 1504; DB 9; Length 273;  
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 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1   | MRGQEVLLMVLVAVGGTEHAYRPGRRVCAVRAHGDVSSSFVQVQPLTTCGDHR      | 60  |
| Qy | 61  | ACSTYRTIYRTAYRRSGLAPARPRYACCPGWKRTSLGACGAAICQPPCRNGSCVOP   | 120 |
| Db | 61  | ACSTYRTIYRTAYRRSGLAPARPRYACCPGWKRTSLGACGAAICQPPCRNGSCVOP   | 120 |
| Qy | 121 | GRCRPAGWRGDTQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG    | 180 |
| Db | 121 | GRCRPAGWRGDTQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG    | 180 |
| Qy | 181 | GPVRVAPNPTGVDSAMKEEVQRLQSRVDLLBEKQLVLAFLHSLASQALEHGLPDPGSL | 240 |
| Db | 181 | GPVRVAPNPTGVDSAMKEEVQRLQSRVDLLBEKQLVLAFLHSLASQALEHGLPDPGSL | 240 |
| Qy | 241 | VHSFOQLGRIDSLSQISFLBEOQLGSCCKDS                            | 273 |
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RESULT 9

US-09-978-192A-508  
 ; Sequence 508, Application US/09978192A  
 ; Patent No. US2002017753A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
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 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
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 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C9  
 ; CURRENT APPLICATION NUMBER: US/09/978,192A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
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 ; PRIOR APPLICATION NUMBER: 60/062250  
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DB 1 MRGSEVLLMMLVLA VGTGTEHAYRPPRRVCAVRAGDPVSEFVQRYVQPLTTCDGR 60  
QY 61 ACSTYRTTYTAVRSPGLAPAPRYAACCGWRRTSGLPACGAALCPPCRNNGSCVQP 120  
DB 61 ACSTYRTTYTAVRSPGLAPAPRYAACCGWRRTSGLPACGAALCPPCRNNGSCVQP 120  
QY 121 GRGCRPAGMRGDTQSDVDECSARRGGCPORCVNTTGSYWCQCBWBSHLSADGTLCPK 180  
DB 121 GRGCRPAGMRGDTQSDVDECSARRGGCPORCVNTTGSYWCQCBWBSHLSADGTLCPK 180  
QY 181 GPRVAPNPTGVDSAMKEEYVORLQSRVDLLEKQLVLAFLHSLASQALEHGLPDGSL 240  
DB 181 GPRVAPNPTGVDSAMKEEYVORLQSRVDLLEKQLVLAFLHSLASQALEHGLPDGSL 240  
QY 241 VHSFOQLGRIDLSSEQISTLEQLGSCSKXDS 273  
DB 241 VHSFOQLGRIDLSSEQISTLEQLGSCSKXDS 273

RESULT 10  
US-09-790-264-10  
Sequence 10, Application US/09790264  
Patent No. US2002028508A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
FILE REFERENCE: 07334-322001  
CURRENT APPLICATION NUMBER: US/09/790,264  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/298,531  
PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/337,930  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: US 09/102,705  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: US 09/363,630  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(22)  
US-09-790-264-10

Query Match 99.9%; Score 1504; DB 10; Length 273;  
Best Local Similarity 99.6%; Pred. No. 1.5e-100;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQEVLLMWLLVAVGGTTHAYRGRVCAVRAHGDVPSFVQRYVQPFLLTTCDGHR 60  
Db 1 MRGQEVLLMWLLVAVGGTTHAYRGRVCAVRAHGDVPSFVQRYVQPFLLTTCDGHR 60

Qy 61 ACSTVRTIYRTAYRRSPGLAPARYACCPGKRTSGLPACGAAICQPPCRNGGSCVQP 120  
Db 61 ACSTVRTIYRTAYRRSPGLAPARYACCPGKRTSGLPACGAAICQPPCRNGGSCVQP 120

Qy 121 GRCPAGWGRDTCOSDVDECSARRGCGPCRCVNTAGSYWCQWEGHSLADGTLCPVK 180  
Db 121 GRCPAGWGRDTCOSDVDECSARRGCGPCRCVNTAGSYWCQWEGHSLADGTLCPVK 180

Qy 181 GPPRVAPNPTGVDSAMKEEVORLSRVLDLEEKQLVLAHLPLHSLASQALEHGLPDPGSL 240  
Db 181 GPPRVAPNPTGVDSAMKEEVORLSRVLDLEEKQLVLAHLPLHSLASQALEHGLPDPGSL 240

Qy 241 VHSFOQLGRIDSLSEQISFLEEQSCCKKDS 273  
Db 241 VHSFOQLGRIDSLSEQISFLEEQSCCKKDS 273

RESULT 11  
US-09-790-264-12  
Sequence 12, Application US/09790264  
Patent No. US2002028508A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES  
FILE REFERENCE: 07334-322001  
CURRENT APPLICATION NUMBER: US/09/790,264  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/298,531  
PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/337,930  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: US 09/102,705  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: US 09/363,630  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-790-264-12

Query Match 92.5%; Score 1392; DB 10; Length 251;  
Best Local Similarity 99.6%; Pred. No. 1.3e-92;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AYRPGRVCAVRAHGDVPSFVQRYVQPFLLTTCDGHRACSTVRTIYRTAYRRSPGLA 82  
Db 1 AYRPGRVCAVRAHGDVPSFVQRYVQPFLLTTCDGHRACSTVRTIYRTAYRRSPGLA 60

Qy 83 RPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWGRDTCOSDVDECS 142  
Db 61 RPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWGRDTCOSDVDECS 120

Qy 143 ARRGCGPCRCVNTAGSYWCQWEGHSLADGTLCPVKGGPPRVAPNPTGVDSAMKEEVOR 202  
Db 121 ARRGCGPCRCVNTAGSYWCQWEGHSLADGTLCPVKGGPPRVAPNPTGVDSAMKEEVOR 180

Qy 203 LQSRVDLLEEKQLVLAHLPLHSLASQALEHGLPDPGSLVHVSFOQLGRIDSLSEQISFLEE 262  
Db 181 LQSRVDLLEEKQLVLAHLPLHSLASQALEHGLPDPGSLVHVSFOQLGRIDSLSEQISFLEE 240

Qy 263 QLGSCSCCKDS 273  
Db 241 QLGSCSCCKDS 251

RESULT 12  
US-09-978-295A-2  
Sequence 2, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



| Query Match   | 89.1%        | Score 1340.5    | DB 9         | Length 295 |        |
|---|--------------|-----------------|--------------|------------|--------|
| Best Local Similarity   | 94.6%        | Pred. No. 78-89 |              |            |        |
| Matches 246   | Conservative | 2               | Mismatches 9 | Indels 3   | Gaps 2 |
| 17 VGTGEHAYR-PGRVCAN--RAHGDPVSESFVQVVTQPFLLTTCDCGHRACSTYRTIYRTAY 73     |              |                 |              |            |        |
| 36 VSGRHRARLPAFLPLGCVLSRAHGDPVSESFVQVVTQPFLLTTCDCGHRACSTYRTIYRTAY 95    |              |                 |              |            |        |
| 74 RRSPLGLAPARPRYACCPGKWTSGTGLPGACGAAICQPPCRNGSCVQPGRCRCFAGWGGDT 133    |              |                 |              |            |        |
| 96 RRSPLGLAPARPRYACCPGKWTSGTGLPGACGAAICQPPCRNGSCVQPGRCRCFAGWGGDT 155    |              |                 |              |            |        |
| 134 COSDVDECSARRGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPRVAPNPTGVD 193     |              |                 |              |            |        |
| 156 COSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSDAGTLCVPGKGGPRVAPNPTGVD 215     |              |                 |              |            |        |
| 194 SAMKEEVQRLQSRVDLLEKQLVLAPLHLSLASQALSHGLPDPGSLLVHVSFQGLGRIDSL 253    |              |                 |              |            |        |
| 216 SAMKEEVQRLQSRVDLLEKQLVLAPLHLSLASQALSHGLPDPGSLLVHVSFQGLGRIDSL 275    |              |                 |              |            |        |
| 254 SQQISFLEQLGSCCKKDS 273  |              |                 |              |            |        |
| 276 SQQISFLEQLGSCCKKDS 295  |              |                 |              |            |        |
| RESULT 13   |              |                 |              |            |        |
| US-09-978-697-2   |              |                 |              |            |        |
| Sequence 2, Application US/09978697                                     |              |                 |              |            |        |
| Patent No. US20020169284A1  |              |                 |              |            |        |
| GENERAL INFORMATION:  |              |                 |              |            |        |
| APPLICANT: Ashkenazi, Avi   |              |                 |              |            |        |
| APPLICANT: Baker Kevin P.   |              |                 |              |            |        |
| APPLICANT: Botstein, David  |              |                 |              |            |        |
| APPLICANT: Descoviers, Luc  |              |                 |              |            |        |
| APPLICANT: Eaton, Dan   |              |                 |              |            |        |
| APPLICANT: Ferrara, Napoleon  |              |                 |              |            |        |
| APPLICANT: Filvaroff, Ellen   |              |                 |              |            |        |
| APPLICANT: Fong, Sherman  |              |                 |              |            |        |
| APPLICANT: Gao, Wei-Qiang   |              |                 |              |            |        |
| APPLICANT: Gerber, Hanspeter  |              |                 |              |            |        |
| APPLICANT: Gerritsen, Mary E.   |              |                 |              |            |        |
| APPLICANT: Goddard, Audrey  |              |                 |              |            |        |
| APPLICANT: Godowski, Paul J.  |              |                 |              |            |        |
| APPLICANT: Grimaldi, J. Christopher                                     |              |                 |              |            |        |
| APPLICANT: Gurney, Austin L.  |              |                 |              |            |        |
| APPLICANT: Hillan, Kenneth J.   |              |                 |              |            |        |
| APPLICANT: Kijavlin, Ivar J.  |              |                 |              |            |        |
| APPLICANT: Kuo, Sophia S.   |              |                 |              |            |        |
| APPLICANT: Napier, Mary A.  |              |                 |              |            |        |
| APPLICANT: Pan, James   |              |                 |              |            |        |
| APPLICANT: Paoni, Nicholas F.   |              |                 |              |            |        |
| APPLICANT: Roy, Margaret Ann  |              |                 |              |            |        |
| APPLICANT: Shelton, David L.  |              |                 |              |            |        |
| APPLICANT: Stewart, Timothy A.  |              |                 |              |            |        |
| APPLICANT: Tumas, Daniel  |              |                 |              |            |        |
| APPLICANT: Williams, P. Mickey  |              |                 |              |            |        |
| APPLICANT: Wood, William I.   |              |                 |              |            |        |
| TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic |              |                 |              |            |        |
| TITLE OF INVENTION: Acids Encoding the Same                             |              |                 |              |            |        |
| FILE REFERENCE: P2630P1C27  |              |                 |              |            |        |
| CURRENT APPLICATION NUMBER: US/09/978,697                               |              |                 |              |            |        |
| CURRENT FILING DATE: 2001-10-16   |              |                 |              |            |        |
| PRIOR APPLICATION NUMBER: 09/918585                                     |              |                 |              |            |        |
| PRIOR FILING DATE: 2001-07-30   |              |                 |              |            |        |
| PRIOR APPLICATION NUMBER: 60/062250                                     |              |                 |              |            |        |
| PRIOR FILING DATE: 1997-10-17   |              |                 |              |            |        |
| PRIOR APPLICATION NUMBER: 60/064249                                     |              |                 |              |            |        |
| PRIOR FILING DATE: 1997-11-03   |              |                 |              |            |        |
| PRIOR APPLICATION NUMBER: 60/065311                                     |              |                 |              |            |        |
| PRIOR FILING DATE: 1997-11-13   |              |                 |              |            |        |

PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.1%; Score 1340.5; DB 9; Length 295;  
Best Local Similarity 94.6%; Pred. No. 76-89; Indels 3; Gaps 2;  
Matches 246; Conservative 2; Mismatches 9;

QY 17 VGGTEHAYR-FGRYCAV--RAHGDVSSFPVRYOPLTTCGHRACSTYRTYRTAY 73  
DB 36 VSGGRHARLPARPLGCVLSRAHGDVSSFPVRYOPLTTCGHRACSTYRTYRTAY 95  
QY 74 RSPGLAPAPRYACCPGMRKTSGLPGAGAAICPPCENGGSCVQPGRCRCPAGMRDPT 133  
DB 96 RSPGLAPAPRYACCPGMRKTSGLPGAGAAICPPCENGGSCVQPGRCRCPAGMRDPT 155  
QY 134 CQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLADGTLCPVPGPVPVAPNPTGVD 193  
DB 156 CQSDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLADGTLCPVPGPVPVAPNPTGVD 215  
QY 194 SAKKEVQRLQSRVLDLEKQLVLAFLHSLASQALEHGLPDGSLVHSPQGLRIDSL 253  
DB 216 SAKKEVQRLQSRVLDLEKQLVLAFLHSLASQALEHGLPDGSLVHSPQGLRIDSL 275  
QY 254 SEQISFLEEQLGSCCKKDS 273  
DB 276 SEQISFLEEQLGSCCKKDS 295

RESULT 14  
US-09-978-192A-2  
Sequence 2, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978, 192A  
CURRENT FILING DATE: 2001-10-15

**us-09-852-472-2.rapb**

PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203

RESULT 15  
 US-09-790-264-15  
 Sequence 15, Application US/09790264  
 Patent No. US2002028508A1  
 GENERAL INFORMATION:  
 APPLICANT: Holtzman, Douglas A.  
 APPLICANT: Goodearl, Andrew D.J.  
 APPLICANT: McCarthy, Sean A.  
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
 TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
 FILE REFERENCE: 07334-322001  
 CURRENT APPLICATION NUMBER: US/09/790,264  
 CURRENT FILING DATE: 2001-02-21  
 PRIOR APPLICATION NUMBER: US 09/065,661  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: US 09/298,531  
 PRIOR FILING DATE: 1999-04-23  
 PRIOR APPLICATION NUMBER: US 09/065,363  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: US 09/337,930  
 PRIOR FILING DATE: 1999-06-22  
 PRIOR APPLICATION NUMBER: US 09/102,705  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: US 09/363,630  
 PRIOR FILING DATE: 1999-07-29  
 PRIOR APPLICATION NUMBER: US 09/124,538  
 PRIOR FILING DATE: 1998-07-29

Search completed: December 17, 2002, 10:09:45  
Job time : 9.80645 secs





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OM protein - protein search, using sw model

Run on: December 17, 2002, 10:00:11 ; Search time 15.0228 Seconds

(without alignments)  
1746.994 Million cell updates/sec

Title: US-09-852-472-2

Perfect score: 1505

Sequence: 1 MRGSQEVLLMMLVAVGCT.....SEQISFLEQLGSCCKKDS 273

Scoring table: BLASTN62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database: 1: PIR 73.1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | ID       | Description                  |
|------------|-------|-------|--------|----------|------------------------------|
| 1          | 434.5 | 28.9  | 293    | 2 T09065 | hypothetical protein - mouse |
| 2          | 257   | 17.1  | 1574   | 2 T13954 | MEGFE protein - rat          |
| 3          | 253.5 | 16.8  | 558    | 2 T17324 | hypothetical prote           |
| 4          | 219   | 14.6  | 1620   | 2 T27283 | hypothetical prote           |
| 5          | 196   | 13.0  | 1964   | 2 T09059 | notch4 - mouse               |
| 6          | 189   | 12.6  | 678    | 2 B48089 | growth arrest-spec           |
| 7          | 184   | 12.2  | 673    | 2 B48089 | growth arrest-spec           |
| 8          | 182.5 | 12.1  | 2907   | 2 A57278 | Nel-homolog protei           |
| 9          | 181   | 12.0  | 810    | 2 T10756 | growth potentialin           |
| 10         | 178   | 11.8  | 674    | 2 I55476 | fibritillin-1 precu          |
| 11         | 175.5 | 11.7  | 3002   | 2 A47221 | notch3 protein - h           |
| 12         | 174.5 | 11.6  | 2321   | 2 S78549 | notch protein - fr           |
| 13         | 174   | 11.5  | 2703   | 1 A24420 | notch protein - fr           |
| 14         | 173.5 | 11.5  | 1247   | 1 MMHUND | notch protein - fr           |
| 15         | 173   | 11.5  | 835    | 2 JP0076 | notch protein - fr           |
| 16         | 172   | 11.4  | 2531   | 2 A46019 | Notch-1 protein -            |
| 17         | 171.5 | 11.4  | 2871   | 2 A55624 | fibritillin-1 precu          |
| 18         | 170.5 | 11.3  | 2871   | 2 A55624 | fibritillin-1 precu          |
| 19         | 170   | 11.3  | 675    | 1 KXMS   | plasma protein S p           |
| 20         | 170   | 11.3  | 2918   | 2 A54105 | plasma protein S p           |
| 21         | 168.5 | 11.2  | 2318   | 2 S45306 | notch 3 protein -            |
| 22         | 168   | 11.2  | 675    | 1 KXRTS  | plasma protein S p           |
| 23         | 168   | 11.2  | 833    | 2 S19087 | gene Delta protein           |
| 24         | 165   | 11.0  | 880    | 2 A31246 | neurogenic protein           |
| 25         | 165   | 11.0  | 880    | 2 S00670 | neurogenic protein           |
| 26         | 165   | 11.0  | 2524   | 2 A35844 | neurogenic protein           |
| 27         | 164   | 10.9  | 1429   | 2 S06434 | neurogenic protein           |
| 28         | 164   | 10.9  | 2555   | 2 A40043 | neurogenic protein           |
| 29         | 163   | 10.8  | 3871   | 2 T22812 | hypothetical prote           |

|    |       |      |      |          |                     |
|----|-------|------|------|----------|---------------------|
| 30 | 162   | 10.8 | 387  | 2 B49175 | Notch A protein -   |
| 31 | 162   | 10.8 | 646  | 2 S38819 | plasma protein S -  |
| 32 | 162   | 10.8 | 675  | 1 KXROS  | plasma protein S p  |
| 33 | 160.5 | 10.7 | 2531 | 2 S18188 | notch protein homo  |
| 34 | 160   | 10.6 | 2437 | 2 S42612 | transmembrane prot  |
| 35 | 159.5 | 10.6 | 407  | 1 KFB07  | coagulation factor  |
| 36 | 159   | 10.6 | 1820 | 2 A55494 | latent transformin  |
| 37 | 158.5 | 10.5 | 456  | 1 KXBO   | protein C (activat  |
| 38 | 157   | 10.4 | 676  | 1 KXHUS  | plasma protein S p  |
| 39 | 157   | 10.4 | 1221 | 2 A49457 | fibritillin-2 precu |
| 40 | 156   | 10.4 | 642  | 2 S53434 | plasma protein S p  |
| 41 | 155.5 | 10.3 | 466  | 1 KFHU7  | coagulation factor  |
| 42 | 155   | 10.3 | 387  | 2 S38449 | extracellular prot  |
| 43 | 154.5 | 10.3 | 1408 | 2 S16148 | gene serrate prote  |
| 44 | 154.5 | 10.3 | 3635 | 2 T10053 | laminin alpha 5 ch  |
| 45 | 154   | 10.2 | 642  | 2 S53433 | plasma protein S p  |

## ALIGNMENTS

### RESULT 1

T09065  
hypothetical protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jan-2000  
C/Accession: T09065  
R/Rowen, L.; Mahatras, G.; Qin, S.; Alharr, M.E.; Dankers, C.; Loretz, C.; Sci  
submitted to the EMBL Data Library, October 1997  
A/Description: Sequence of the mouse major histocompatibility locus class III region.  
A/Reference number: Z16543  
A/Accession: T09065  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-293 <ROW>  
A/Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564953  
C/Genetics:  
A/Map position: 17  
A/Intons: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3; 280/1  
C/Superfamily: unassigned EGF-related proteins; EGF homology  
F:114-141/Domain: EGF homology <EGF1>  
F:148-183/Domain: EGF homology <EGF>

Query Match 28.9%; Score 434.5; DB 2; Length 293;  
Best Local Similarity 37.3%; Pred. No. 1.1e-24;

Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MRGSQEVLLMMLVAVG-GTE-HAYRGRVCAVRAHGPV--SESFVQRYQPFITTC     | 56  |
| DB | 11  | LRG-----LSFVLVMTGEGTGSGFKESLIGVSKOTLLVPLRVNESYSQPVYKPYLTLC | 65  |
| QY | 57  | DGHRACSTRTITRTAYRSPGLARPRVACCPGKRTSGLPACGA-AICQPPCRNGG     | 115 |
| DB | 66  | ARRRISCTRTITRTAYRSPGLARPRVACCPGKRTSGLPACGA-AICQPPCRNGG     | 122 |
| QY | 116 | SCVQGRGRCPCAGNRGDDCQSDVDECSARRGCPQRCVNTASGYWCQEGHSADGTL    | 175 |
| DB | 123 | VCTGDRBCACAGNGKCHVDVDECRASLTLCGHCINTIGSFPCPHPLVGLDRT       | 182 |
| QY | 176 | CVPKGGPPVAVNPPTGV-----DSMKKEVQLGRVLLERKQLVLAFL             | 221 |
| DB | 183 | CA--GGPPE--SPTSASILSAVAREADSEERALLRWEALRGLRLEQ-----        | 228 |
| QY | 222 | HSLASQA---LEHGLP-DPGSLVHSFOQL-----GRIDSSEQISFLEQSGSCCKKDS  | 273 |
| DB | 229 | --WATQAGWRAVAVLPMPEELRPEQVAVELMGDRRLISLSDQVLLERKQACACEDNS  | 286 |

### RESULT 2

T13954  
MEGFE protein - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000



Mol. Cell. Biol. 13, 4976-4985, 1993  
A>Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730  
A:Accession: B48089  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-678 <MAN>

A:Cross-references: GB:L13720; NID:9401766; PIDN:AAA58494.1; PID:9401767  
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom  
F:120-153/Domain: EGF homology <EG1>  
F:160-195/Domain: EGF homology <EG2>  
F:201-236/Domain: EGF homology <EG3>  
F:242-277/Domain: EGF homology <EG4>  
F:311-671/Domain: sex hormone-binding globulin homology <SHB>  
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match  
Best Local Similarity 12.6%; Score 189; DB 2; Length 678;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRVQPFLLTCDGH-----RACSTYRTTYTAYRSPGLAPAPRYACC-----FGWK 93  
DB 47 RRAVQVFEAKQGHLEBCEVEELCS--REAEVEFENDPETDYPRYLDCINKYSGPYT 104  
QY 94 RTSG-----LPAGCAATCOPPC-RNGSGCVP--GR--CRCPAGMRDPTCQSDVDEC 141  
DB 105 KNGSFATCVQNLPDCC---TNPDCRKGTOACQDLMNFECLCKAKWGRLDKDVNEC 160  
QY 142 SARRGCPQRCVNTAGSYWCQCBGHSLSADGTLG 176  
DB 161 SQENGCCIQICNKGKSFHCSGHSFELSSDGRYC 195

## RESULT 7

A48089  
Growth arrest-specific protein gas6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999  
C:Accession: A48089; S37437  
R:Manfioletti, G.; Biancolini, C.; Avanzi, G.; Schneider, C.  
Mol. Cell. Biol. 13, 4976-4985, 1993  
A>Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730  
A:Accession: A48089  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-673 <MAN>

A:Cross-references: GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061  
A:Note: authors translated the codon CCC for residue 424 as Ile  
C:Genetics:  
A:Gene: gas6  
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom

F:38-89/Domain: Glu domain homology #status atypical <GLA>  
F:117-150/Domain: EGF homology <EG1>  
F:157-199/Domain: EGF homology <EG2>  
F:198-233/Domain: EGF homology <EG3>  
F:239-274/Domain: EGF homology <EG4>  
F:308-666/Domain: sex hormone-binding globulin homology <SHB>  
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match  
Best Local Similarity 12.2%; Score 184; DB 2; Length 673;  
Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

QY 46 QRVQPFLLTCDGH-----RACSTYRTTYTAYRSPGLAPAPRYACC-----89  
DB 44 RRAVQVFEAKQGHLEBCEVEELCSKEA--REVEFNDPETDYPRYLDCINKYSGPEE 101  
QY 90 --PGW-KRTSGLPAC-----GALICQPCRNKSGCVPGRCRCPAGMRDPTCQSDV 138

DB 102 KNDFPACVQNLPDQCTPNPCDKGTHIQDLMGN-----PFCVCTDGMGRLCDKDV 154  
QY 139 DECSARRGCGPCVNTAGSYWCQCBGHSLSADGTLG 176  
DB 155 NECVQKNGGCGVCHNKFGSFQCHSGSGLASDQTC 192

## RESULT 8

A57278  
fibrillin-2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 02-Aug-2002  
R:Zhang, H.; Hu, W.; Ramirez, F.  
J. Cell Biol. 129, 1165-1176, 1995  
A>Title: Developmental expression of fibrillin genes suggests heterogeneity of extracelli  
A:Reference number: A57278; MUID:95263670; PMID:7744963  
A:Accession: A57278  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2907 <ZHA>  
A:Cross-references: GB:L39790; NID:9762830; PIDN:AAA74908.1; PID:9762831  
C:Superfamily: fibrillin 1; EGF homology  
F:139-1274/Domain: EGF homology <EGF1>  
F:2488-2523/Domain: EGF homology <EGF>

Query Match  
Best Local Similarity 12.1%; Score 182.5; DB 2; Length 2907;  
Matches 59; Conservative 20; Mismatches 85; Indels 87; Gaps 7;

QY 2 RGSQEVLLMWLVAVGTEHAY-----RPGRRVCAVBAHGPVSESPVQVYQPFLLT 54  
DB 77 RQQDELIRG--PNVCGSRFHSYCCPGWKTLPGNQGIVETICNAGDEFCR--PNMC 130  
QY 55 TCDGHRACST--YRTTYTAYRSPGLAPAPRYACCPCGKRTSGLPAGCAATCQPCR 112  
DB 131 TSSGQISPTGGRKSIQCCSVRCMNGSTCADHDQCCQKGYTF-----YCGQPVENGCG 185  
QY 113 NCGSCVQGRRCRCPCAGMRDPTCQ-----135  
DB 166 NGRCLGPNRCACVGTGPGQCEEDYRTGCPFYVNNMCQCGQLGIYCTKTLCCATTGR 245  
QY 136 -----SDVDEGARRGCP--GRCVNTAGSYWCQCE 165  
DB 246 AMGHPCEWCPAQPCRGRTPIPIRTGACQDVEDCOAIPGLCGGNCINTVGSFECRCPA 305  
QY 166 GHSLSADGTLG 176  
DB 306 GHKQSETTQRC 316

## RESULT 9

T10756  
Nel-homolog protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
R:Kuroda, S.; Yokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsushashi, S.; Kikkawa, U.  
submitted to the EMBL Data Library, November 1998  
A:Description: Protein kinase C-binding protein.  
A:Reference number: Z17122  
A:Accession: T10756  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-810 <KUR>  
A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180  
A:Experimental source: strain Sprague-Dawley, brain

Query Match  
Best Local Similarity 12.0%; Score 181; DB 2; Length 810;  
Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 88 CPGWKRTSGLPACGAATCOPPCRNKSGCVPGRCRCPAGMRDPTCQSDVDECSARRG 147



## RESULT 12

S78549

notch3 protein - human

C/Species: Homo sapiens (man)

C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Aug-2002

C/Accession: S78549; S71825

R/Journal: A.; Tournier-Lasserre, E.

A/Reference number: S78549

A/Accession: S78549

A/Molecule type: mRNA

A/Residues: 1-2321 &lt;COU&gt;

A/Cross-references: EMBL:U97669; NID:92668591; PIDN:AAE91371.1; PID:92668592

R/Journal: A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabiriat, H.; Mouton, F.; Alamowicz

Nature 383, 707-710, 1996

A/Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke

A/Reference number: S71825; PMID:97032728; PMID:8878478

A/Accession: S71825

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 67-113,138-194,268-333, 'G', 335-346,536-613,716-765,1240-1279,1815-1868 &lt;UOUZ

A/Cross-references: EMBL:U97669

C/Genetics:

A/Gene: notch3

A/Map position: 19p13.1

C/Function:

A/Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and

C/Keywords: tandem repeat; EGF homology; EGF homology; laminin-type EGF-1

F/123-155/Domain: EGF homology &lt;EGX1&gt;

F/162-194/Domain: EGF homology &lt;EGX1&gt;

F/240-271/Domain: EGF homology &lt;EGX2&gt;

F/318-349/Domain: EGF homology &lt;EGX2&gt;

F/473-504/Domain: EGF homology &lt;EGX3&gt;

F/853-884/Domain: EGF homology &lt;EGX3&gt;

F/928-959/Domain: EGF homology &lt;EGX3&gt;

F/1070-1122/Domain: EGF homology &lt;EGX4&gt;

F/1898-1870/Domain: laminin-type EGF-like homology &lt;LEG&gt;

F/1871-1903/Domain: ankyrin repeat homology &lt;AN1&gt;

F/1805-1937/Domain: ankyrin repeat homology &lt;AN2&gt;

F/1938-1970/Domain: ankyrin repeat homology &lt;AN3&gt;

F/1971-2003/Domain: ankyrin repeat homology &lt;AN5&gt;

Query Match

Best Local Similarity 11.6%; Score 174.5; DB 2; Length 2321;

Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY 56 CDGHRACSTYRTYRTAVRSPGLAPAPRYAC-CPGMRK--TSGLRGACGAATCOPPCR 112

DB 87 CAGRGCCS-----SVAGTARFSCRCRPFGRGPDCLPDC-----ISSPCA 129

QY 113 NGGSC-VDP-GR--CRCPAGMRGDTCCSDVDEC-----SARRGCGPQRCVNTAGSYWCQW 164

DB 130 HCARSTVGPDRFLCSPCPGCGSCSDVDECRCVGEPCRHG--TCLNTPGSRFCQCP 166

QY 165 EGHSLASDGLTCVPGKGPVAVNP 189

DB 187 AGYT-----GFLCENPVP--CAPSP 205

RESULT 13

A24420

Notch protein - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: A24420; A24768; S09358; A05267

R/Journal: S.; Kelley, M.R.; Young, M.W.

Mol. Cell. Biol. 6, 3094-3108, 1986

A/Reference number: A24420; PMID:87064624; PMID:3097517

A/Accession: A24420

A/Molecule type: DNA

A/Residues: 1-2703 &lt;KID&gt;

A/Cross-references: GB:K03508; NID:9157991; PIDN:AAA28725.1; PID:9157993

R/Wharton, K.A.; Johansen, K.M.; Xu, T.; Aravanis-Tsakonas, S.

Cell 43, 567-581, 1985

A/Reference number: A24768; PMID:86079539; PMID:395325

A/Accession: A24768

A/Molecule type: mRNA

A/Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R', 960-1000

A/Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044

Nucleic Acids Res. 17, 6463-6471, 1989

A/Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers

A/Reference number: S09358; PMID:89385974; PMID:2780284

A/Accession: S09358

A/Molecule type: DNA

A/Residues: 2505-2551, 'QQQQ', 2552-2576, 'E', 2578-2604, 'TRU&gt;

R/Wharton, K.A.; Yedvobnick, B.; Finerly, V.G.; Aravanis-Tsakonas, S.

Cell 40, 55-62, 1985

A/Title: opa: a novel family of transcribed repeats shared by the Notch locus and other c

A/Reference number: A05267; PMID:8509329; PMID:2981631

A/Accession: A05267

A/Molecule type: DNA

A/Residues: 2504-2576, 'E', 2578-2611 &lt;MHA2&gt;

C/Genetics:

A/Gene: notch; opa

A/Cross-references: FlyBase:FBgn0004647

A/Map position: 8.96-9.36

A/Intons: 53/3; 84/3; 171/3; 240/3; 283/3; 233/3; 2436/3; 2588/3

C/Superfamily: notch protein; ankyrin repeat homology; EGF homology

C/Keywords: differentiation; tandem repeat; transmembrane protein

F/297-328/Domain: transmembrane #status predicted &lt;TM1&gt;

F/530-561/Domain: EGF homology &lt;EGX1&gt;

F/568-599/Domain: EGF homology &lt;EGX1&gt;

F/968-1019/Domain: EGF homology &lt;EGX2&gt;

F/1064-1095/Domain: EGF homology &lt;EGX3&gt;

F/1187-1218/Domain: EGF homology &lt;EGX3&gt;

F/1746-1762/Domain: transmembrane #status predicted &lt;TM2&gt;

F/1950-1982/Domain: ankyrin repeat homology &lt;AN1&gt;

F/1983-2015/Domain: ankyrin repeat homology &lt;AN2&gt;

F/1988-2004/Domain: transmembrane #status predicted &lt;TM3&gt;

F/2017-2049/Domain: ankyrin repeat homology &lt;AN3&gt;

F/2050-2082/Domain: ankyrin repeat homology &lt;AN4&gt;

F/2083-2115/Domain: ankyrin repeat homology &lt;AN5&gt;

F/2538-2568/Region: glutamine-rich

F/2538-2568/Domain: neurogenic repetitive element #status predicted &lt;OPA&gt;

Query Match

Best Local Similarity 11.6%; Score 174; DB 1; Length 2703;

Matches 60; Conservative 18; Mismatches 67; Indels 76; Gaps 13;

QY 18 GTEHAYRPRRRYAVRAH--GDPVSEFVQRYQPLTTCGHRACSTYRTYRTAYR 75

DB 70 GGTCTVQNGKTKYACADSHYVD-----YCEHRNPQNSMR--CQNGCTCQVTFRNG 118

QY 76 SPGLAPAPRYAC-CP-GMKRT--SGLRGACGAATC----- 107

DB 119 HPGI-----SKCPLGFDLSCEIAVPNACHVTCUNGTCQLTTEBYTCACANGYT 171

QY 108 -----OPCRNGSCV-----QPRCRCPAGMRGDTCCSDVDECSEA---RRGC 148

DB 172 GRCETKYLKASSPCKNATTTALAGSSFTGSCPPGFGDTCSDVDECSSNPKYGG- 230

QY 149 PRCVNTAGSYWCOCBGSLSADGTLTCVPGKGPVAVNP 189

DB 231 --TCVNTAGSYWCOCPTGYT-----GKDCDTKYKP--CBSPSP 263

## RESULT 14

MMHUND

nidogen precursor - human

N/Alternate names: entactin

C/Species: Homo sapiens (man)

Tue Dec 17 14:03:51 2002

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Oct-2000  
 C/Accession: A33322; A32437; A61367  
 R/Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlton  
 DNA 8, 581-594, 1989  
 A/Title: Human nidogen: complete amino acid sequence and structural domains deduced from  
 A/Reference number: A33322; MUID:90091745; PMID:2574658  
 A/Accession: A33322  
 A/Molecule type: mRNA  
 A/Residues: 1-1247 <NAG>  
 A/Cross-references: EMBL:M30269  
 R/Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattel, M.G.; Passage, E.; Weil, D.; Timpl, R.;  
 Am. J. Hum. Genet. 44, 876-885, 1989  
 A/Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to ch  
 A/Reference number: A32437; MUID:89270475; PMID:2471408  
 A/Accession: A32437  
 A/Molecule type: mRNA  
 A/Residues: 667-1247 <OLS>  
 A/Cross-references: EMBL:M27445; NID:9602466; PID:AA57261.1; PID:G602467  
 A/Note: the authors translated the cDNA AAG for residue 966 as Cys  
 R/Pazio, M.J.; O'Leary, J.; Kaehaeri, V.M.; Chen, Y.Q.; Saitta, B.; Utto, J.  
 J. Invest. Dermatol. 97, 281-285, 1991  
 A/Title: Human nidogen: structural and functional characterization of the 5'-flanki  
 A/Reference number: A61367; MUID:91302882; PMID:1906509  
 A/Accession: A61367  
 A/Molecule type: DNA  
 A/Residues: 1-28 <FAZ>  
 C/Comment: This protein is a basement membrane glycoprotein that forms a complex with la  
 C/Genetics:  
 A/Gene: GDB:NID  
 A/Cross-references: GDB:120236; OMIM:131390  
 A/Map position: 1q43-1q43  
 C/Superfamily: nidogen; EGF homology; LDL receptor WYTD-containing repeat homology; thyr  
 C/Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; co  
 protein  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-1247/Product: nidogen #status predicted <MAT>  
 F:290-425/Domain: EGF homology <EG1>  
 F:672-708/Domain: EGF homology <EG2>  
 F:702-704/Region: cell attachment (R-G-D) motif  
 F:714-750/Domain: EGF homology <EG3>  
 F:762-800/Domain: EGF homology <EG4>  
 F:806-839/Domain: EGF homology <EG5>  
 F:849-919/Domain: thyroglobulin type I repeat homology <THY1>  
 F:930-1032/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
 F:1033-1075/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
 F:1076-1120/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
 F:1121-1160/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
 F:1161-1197/Domain: LDL receptor WYTD-containing repeat homology <YW5>  
 F:1212-1243/Domain: EGF homology <EG6>  
 F:289,296/Binding site: sulfate (Tyr) (covalent) #status predicted  
 F:729,819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F:756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin)  
 F:1137/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 11.5%; Score 173.5; DB 1; Length 1247;  
 Best Local Similarity 25.8%; Pred. No. 4.7e-05;  
 Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;  
 QY 20 TEHAYRPPGRV-----CAVRAG-----DPVSEFVRVYQPELTTCGHRACSTYR 66  
 Db 681 TNAACRPGPRTQTCESIGFRGDGRTCDVIDECSE-----QP--SVCSHTICNNH- 730  
 QY 67 TIVTAYRRSPGLAPARPYACPGWKRTSGLPAGACGAAICQPP-----CRNG----- 114  
 Db 731 -----PGTFRCECEGVQFSD--EGTCVAVVDQRPINVCETGLHNCIDIPOR 774  
 QY 115 GSCVQPG-----RCRCPAGWRGD--TCQSDVDECSARRGCGPCORCVNTAGSYWCOCWEHGS 168  
 Db 775 AQCIYTGSSYTCCLPFGSDGOACQ-DVDECQPSRCHPDFAFCNTFTGSGTCCCKPGY- 832  
 QY 169 LSADGTLCLVP-----KGGPRVPANPTG----- 191  
 Db 833 -QGDGFRCPVGEVEKTRQHERHILGAAGATDPQRPPIPPGLFVPECDAGHYAFTQCHG 891

QY 192 -----VDSAKKEEYQRLQSRVLDLEKQLVLAPLH-SLASQALEHGLPDPGSLIVHS 243  
 Db 892 STGYCWCVDGR-EVEGTRTPGWTTPCLSTVAPPIHGGFAVPTAVIPLP-PGTHLL-- 947  
 QY 244 FQQLGRIDSL 253  
 Db 948 PAQTGKIERL 957  
 RESULT 15  
 JP0076  
 nel protein - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 13-Aug-1999  
 C/Accession: A38963; JP0076  
 R/Matsushashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K  
 Dev. Dyn. 203, 212-222, 1995  
 A/Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly ex  
 A/Reference number: A38963; MUID:95383734; PMID:7655083  
 A/Accession: A38963  
 A/Molecule type: mRNA  
 A/Residues: 1-835 <MAT>  
 A/Cross-references: DDBJ:D45365  
 A/Experimental source: 9-day embryo  
 R/Matsushashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K  
 submitted to JIPID, January 1995  
 A/Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is str  
 A/Reference number: JP0076  
 A/Accession: JP0076  
 A/Molecule type: mRNA  
 A/Residues: 1-835 <MA2>  
 A/Cross-references: DDBJ:D45365  
 A/Experimental source: 9-day embryo  
 C/Superfamily: von Willebrand factor type C repeat homology; EGF homology  
 F:273-333/Domain: von Willebrand factor type C repeat homology <WVC>  
 F:395-592/Region: EGF-like repeats  
 F:444-480/Domain: EGF homology <EGF1>  
 F:486-521/Domain: EGF homology <EGF2>  
 F:525-552/Domain: EGF homology <EGF2>  
 Query Match 11.5%; Score 173; DB 2; Length 835;  
 Best Local Similarity 41.4%; Pred. No. 3.6e-05;  
 Matches 29; Conservative 12; Mismatches 27; Indels 2; Gaps 1;  
 QY 100 GACGAATCQPPCRNGGSCVQGRRCRCRCPAGWRGDTQSDVDECSARRGCGPCOR--CVNTAG 157  
 Db 518 GTVCKAFKCKGCRNGACIASNVACAPQCGFTGSPCETDIDECSDGFGVCDGRANCINLP 577  
 QY 158 SYWCQCWEH 167  
 Db 578 WHCECRDGY 587  
 Search completed: December 17, 2002, 10:03:37  
 Job time : 19.0228 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 09:45:16 ; Search time 8.80645 Seconds

Title: US-09-852-472-2  
Perfect score: 1505

Scoring table: BLOSUM62

Searched: 112892 seqs, 41476328 residues

total number of hits satisfying chosen parameters: 112892

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID         | Description         |
|------------|-------|-------------|--------|----|------------|---------------------|
| 1          | 196   | 13.0        | 1964   | 1  | NTC4_MOUSE | P31695 mus musculi  |
| 2          | 188.5 | 12.5        | 2003   | 1  | NTC4_HUMAN | O99466 homo sapien  |
| 3          | 184   | 12.2        | 816    | 1  | NEL2_MOUSE | O61220 mus musculi  |
| 4          | 183   | 12.2        | 810    | 1  | NEL1_HUMAN | O92832 homo sapien  |
| 5          | 182.5 | 12.1        | 2907   | 1  | FBN2_MOUSE | O61535 mus musculi  |
| 6          | 181.5 | 12.1        | 816    | 1  | NEL2_HUMAN | O99435 homo sapien  |
| 7          | 181   | 12.0        | 810    | 1  | NEL1_RAT   | O62919 rattus norv  |
| 8          | 179.5 | 11.9        | 816    | 1  | NEL2_RAT   | O62918 rattus norv  |
| 9          | 176   | 11.7        | 652    | 1  | CD93_HUMAN | O99473 homo sapien  |
| 10         | 176   | 11.7        | 2703   | 1  | NOTC_DROME | E07207 drosophila   |
| 11         | 175.5 | 11.7        | 816    | 1  | NEL_CHICK  | O90827 gallus gal   |
| 12         | 175.5 | 11.7        | 2871   | 1  | FBN1_HUMAN | P35555 homo sapien  |
| 13         | 174.5 | 11.6        | 2321   | 1  | NTC3_HUMAN | O9um47 homo sapien  |
| 14         | 173.5 | 11.5        | 1247   | 1  | NIDO_HUMAN | P14543 homo sapien  |
| 15         | 172   | 11.4        | 2531   | 1  | NTC1_MOUSE | Q01705 mus musculi  |
| 16         | 171.5 | 11.4        | 2871   | 1  | FBN1_MOUSE | O61554 mus musculi  |
| 17         | 170.5 | 11.3        | 2871   | 1  | FBN1_BOVIN | P98133 bos taurus   |
| 18         | 170   | 11.3        | 675    | 1  | PRTS_MOUSE | O08761 mus musculi  |
| 19         | 170   | 11.3        | 2911   | 1  | FBN2_HUMAN | P35556 homo sapien  |
| 20         | 169.5 | 11.3        | 2871   | 1  | FBN1_PIG   | O9rv36 sus scrofa   |
| 21         | 168.5 | 11.2        | 2318   | 1  | NTC3_MOUSE | O61982 mus musculi  |
| 22         | 168   | 11.2        | 675    | 1  | PRTS_RAT   | P53811 rattus norv  |
| 23         | 168   | 11.2        | 833    | 1  | DL_DROME   | P10041 drosophila   |
| 24         | 166   | 11.0        | 1238   | 1  | JAG2_HUMAN | O9y219 homo sapien  |
| 25         | 166   | 11.0        | 1247   | 1  | JAG3_MOUSE | O94765 mus musculi  |
| 26         | 165   | 11.0        | 1202   | 1  | JAG3_RAT   | O9y607 rattus norv  |
| 27         | 165   | 11.0        | 2524   | 1  | NOTC_XENLA | P21783 xenopus lae  |
| 28         | 164   | 10.9        | 1429   | 1  | LIL2_CAEEL | P14588 caenorhabdi  |
| 29         | 163   | 10.8        | 2556   | 1  | NTC1_HUMAN | P46531 homo sapien  |
| 30         | 162   | 10.8        | 644    | 1  | CD93_MOUSE | O89103 mus musculi  |
| 31         | 162   | 10.8        | 646    | 1  | PRTS_RABIT | P98118 coryctolagus |
| 32         | 162   | 10.8        | 675    | 1  | PRTS_BOVIN | P07224 bos taurus   |
| 33         | 161.5 | 10.7        | 618    | 1  | DL13_HUMAN | O9ny37 homo sapien  |

## ALIGNMENTS

|    |       |      |      |   |             |        |              |
|----|-------|------|------|---|-------------|--------|--------------|
| 34 | 161.5 | 10.7 | 2319 | 1 | NTC3_RAT    | O9rl12 | rattus norv  |
| 35 | 161   | 10.7 | 459  | 1 | PRRC_PIG    | O9gl22 | sus scrofa   |
| 36 | 160.5 | 10.7 | 663  | 1 | CD93_FAT    | O9et61 | rattus norv  |
| 37 | 160.5 | 10.7 | 2531 | 1 | NTC1_RAT    | O07008 | rattus norv  |
| 38 | 160   | 10.6 | 2437 | 1 | NTC1_BRAE   | P46530 | brachydanto  |
| 39 | 159.5 | 10.6 | 407  | 1 | FAY_BOVIN   | P22457 | bos taurus   |
| 40 | 158.5 | 10.5 | 456  | 1 | PRYC_BOVIN  | P00745 | bos taurus   |
| 41 | 157.5 | 10.5 | 379  | 1 | WIRI_MOUSE  | O9wnu1 | mus musculus |
| 42 | 157   | 10.5 | 676  | 1 | PRRS_HUMAN  | P07225 | homo sapien  |
| 43 | 157   | 10.4 | 1221 | 1 | FBIL2_MOUSE | P37889 | mus musculus |
| 44 | 156   | 10.4 | 649  | 1 | PRRS_TACUAC | O28502 | macaca mula  |
| 45 | 156   | 10.4 | 1213 | 1 | UAG3_BRAE   | O90y54 | brachydanto  |

## RESULT. 1

ID NCNA MOUSE STANDARD; RT; 1964 AA  
 AC P1655; Q62389; Q62390; Q35442; Q9RLW9; Q88316; Q9RLX0;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1993 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
 DE [contains: Transforming protein Int-3].  
 DE NOTCH4 OR INT3 OR INT-3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92194507; PubMed=1312643;  
 RA Robbins J., Blondel B.J., Gallahan D., Gallahan R.;  
 RT "Mouse mammary tumor gene int-3: a member of the notch gene family  
 RT transforms mammary epithelial cells.";  
 RL J. Virol. 66:2594-2599(1992).  
 RN [2]  
 RP REVISIONS, SEQUENCE FROM N.A.  
 RA MEDLINE=97294599; PubMed=9150355;  
 RA Gallahan D., Gallahan R.;  
 RT "The mouse mammary tumor associated gene INT3 is a unique member of  
 RT the NOTCH gene family (NOTCH4).";  
 RL Oncogene 14:1883-1890(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Lung, and Testis;  
 RC MEDLINE=96281668; PubMed=8681805;  
 RA Uytendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;  
 RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial  
 RT cell-specific mammalian Notch gene.";  
 RL Development 122:2251-2259(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Bowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackone K., Hood L.;  
 RT "Sequence of the mouse major histocompatibility locus class III  
 RT region.";  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1436-1600 FROM N.A.  
 RA MEDLINE=99252212; PubMed=1023382;  
 RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;  
 RT "Intracisternal type A particle-mediated activation of the Notch4/int3  
 RT gene in a mouse mammary tumor: generation of truncated Notch4/int3  
 RT mRNAs by retroviral splicing events.";  
 RL J. Virol. 73:5166-5171(1999).  
 RN [6]  
 RP FUNCTION.  
 RA MEDLINE=21244657; PubMed=11344305;  
 RA Uytendaele H., Ho J., Rosant J., Kitajewski J.;  
 RT "Vascular patterning defects associated with expression of activated

RT Notch4 in embryonic endothelium.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).  
 RP [7]  
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS  
 OF VAL-1463.  
 RA MEDLINE=21523956; PubMed=11518718;  
 RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
 RT "Marine notch homologs (NL-4) undergo presenilin-dependent  
 proteolysis.";  
 RL J. Biol. Chem. 276:40268-40273(2001).  
 RN [8]  
 RN POST-TRANSLATIONAL PROCESSING.  
 RX MEDLINE=21374376; PubMed=11459941;  
 RA Mitutani T., Taniuchi Y., Aoki T., Hashimoto N., Honjo T.;  
 RT "Conservation of the biochemical mechanisms of signal transduction  
 among mammalian Notch family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 upon ligand activation through the released notch intracellular  
 domain (NICD) it forms a transcriptional activator complex with  
 RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 apoptotic programs (By similarity). May regulate branching  
 morphogenesis in the developing vascular system.  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 terminal fragment N(EC) which are probably linked by disulfide  
 bonds.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart  
 kidney, and at lower levels in the ovary and skeletal muscle. A  
 very low expression is seen in the brain, intestine, liver and  
 testis.  
 CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during  
 embryonic development from 9.0 d.p.c.  
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 which is proteolytically cleaved by a furin-like convertase in the  
 trans-Golgi network before it reaches the plasma membrane to yield  
 an active, ligand-accessible form. Cleavage results in a C-  
 terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 ligand binding, it is cleaved by TNF-alpha converting enzyme  
 (TACE) to yield a membrane-associated intermediate fragment called  
 notch extracellular truncation (NEXT). This fragment is then  
 cleaved by presenilin dependent gamma-secretase to release a  
 notch-derived peptide containing the intracellular domain (NICD)  
 from the membrane.  
 CC -!- PTM: Phosphorylated.  
 CC -!- DISEASE: Loss of the extracellular domain causes constitutive  
 activation of the Notch protein, which leads to hyperproliferation  
 of glandular epithelial tissues and development of mammary  
 carcinomas.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M00456; AAB38377.1; -;  
 DR EMBL; U43691; AAC2630.1; -;  
 DR EMBL; U43691; AAC2631.1; -;  
 DR EMBL; AF030001; AAB82004.1; -;  
 DR EMBL; AB016771; BAA32281.1; ALT SEQ.  
 DR EMBL; AB016772; BAA32283.1; ALT INIT.  
 DR EMBL; AB016773; BAA32284.1; ALT\_INIT.  
 DR EMBL; AB016774; BAA32285.1; -;

PIR; A38072; TVMVT3.  
 HSSP; P08709; LBF9.  
 MGI; 107471; Notch4.  
 InterPro; IPR002110; ANK.  
 InterPro; IPR000152; Asx hydroxyl.  
 InterPro; IPR000561; EGF-like.  
 InterPro; IPR000742; EGF\_2.  
 InterPro; IPR001881; EGF-Ca.  
 InterPro; IPR001438; EGF-II.  
 InterPro; IPR000800; Notch.  
 Pfam; PF00008; EGF; 27.  
 Pfam; PF00023; ank; 6.  
 Pfam; PF00066; notch; 2.  
 PRINTS; PR01415; ANKYRIN.  
 PRINTS; PR00010; EGFBLD.  
 PRINTS; PR01452; NOTCH.  
 SMART; SM00248; ANK; 5.  
 SMART; SM00179; EGF\_CA; 11.  
 SMART; SM00001; EGF\_like; 15.  
 SMART; SM00004; NL; 2.  
 PROSITE; PS00088; ANK\_REPEAT; 5.  
 PROSITE; PS02097; ANK\_REPEAT\_REGION; 1.  
 PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 PROSITE; PS00022; EGF\_1; 28.  
 PROSITE; PS01186; EGF\_2; 21.  
 PROSITE; PS01187; EGF\_CA; 9.  
 Receptor; Transcription regulation; Activator; Differentiation;  
 Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.  
 SIGNAL 1 20  
 CHAIN 21 1964 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.  
 CHAIN 1411 1964 TRANSFORMING PROTEIN INT-3.  
 CHAIN 1428 1964 NOTCH EXTRACELLULAR TRUNCATION.  
 CHAIN 1463 1964 NOTCH INTRACELLULAR DOMAIN.  
 DOMAIN 21 1443 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 1444 1464 POTENTIAL.  
 DOMAIN 1465 1964 CYTOPLASMIC (POTENTIAL).  
 DOMAIN 21 60 EGF-LIKE 1.  
 DOMAIN 61 112 EGF-LIKE 2.  
 DOMAIN 115 152 EGF-LIKE 3.  
 DOMAIN 153 189 EGF-LIKE 4.  
 DOMAIN 191 229 EGF-LIKE 5.  
 DOMAIN 231 271 EGF-LIKE 6.  
 DOMAIN 273 309 EGF-LIKE 7.  
 DOMAIN 311 350 EGF-LIKE 8.  
 DOMAIN 352 388 EGF-LIKE 9.  
 DOMAIN 389 427 EGF-LIKE 10.  
 DOMAIN 429 470 EGF-LIKE 11.  
 DOMAIN 472 508 EGF-LIKE 12.  
 DOMAIN 510 546 EGF-LIKE 13.  
 DOMAIN 548 584 EGF-LIKE 14.  
 DOMAIN 586 622 EGF-LIKE 15.  
 DOMAIN 623 656 EGF-LIKE 16.  
 DOMAIN 658 686 EGF-LIKE 17.  
 DOMAIN 688 724 EGF-LIKE 18.  
 DOMAIN 726 762 EGF-LIKE 19.  
 DOMAIN 764 800 EGF-LIKE 20.  
 DOMAIN 803 839 EGF-LIKE 21.  
 DOMAIN 841 877 EGF-LIKE 22.  
 DOMAIN 878 924 EGF-LIKE 23.  
 DOMAIN 926 962 EGF-LIKE 24.  
 DOMAIN 964 1000 EGF-LIKE 25.  
 DOMAIN 1002 1040 EGF-LIKE 26.  
 DOMAIN 1042 1081 EGF-LIKE 27.  
 DOMAIN 1083 1122 EGF-LIKE 28.  
 DOMAIN 1126 1167 EGF-LIKE 29.  
 REPEAT 1168 1208 LIN/NOTCH 1.  
 REPEAT 1209 1242 LIN/NOTCH 2.  
 REPEAT 1243 1282 LIN/NOTCH 3.  
 REPEAT 1283 1322 ANK 1.  
 REPEAT 1323 1363 ANK 2.  
 REPEAT 1364 1404 ANK 3.  
 REPEAT 1405 1445 ANK 4.



Query Match 13.0%; Score 196; DB 1; Length 1964;  
 Best Local Similarity 34.2%; Pred. No. 1.7e-07;  
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

80 APPRRACGKMK-RISGPGAGCAICPPORNGSCVCPG---RCPCPGMRDPTQ 135  
 134 ASRPGSCGPGMTGEOCQIRFCSA---NPCANGVCLATYPTQICRCPPGEGHTCE 189  
 136 SDVDECSARRGGPQ--RCVNTAGSYWCQ---WEGHSLADTLCP---KGGPRVA 186  
 190 RDINEGFLBPGPCCPGSCNNTIGSYGCLCPVQGBPGCKLRGACPPGSCNNGTCQLV 249  
 187 PNP-----TGVDANKKEE 199  
 250 PEGHSTFHLCLCPPGFTLDCENMPD 275

RESULT 2  
 NTCH4\_HUMAN STANDARD; PRT; 2003 AA.  
 AC Q99466; Q00306; Q99940; Q99458; Q9H3S8; Q9UI19; Q9UIJ0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
 DE (Mnorch4).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX [1] SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.  
 RC TISSUE=Placenta;  
 MEDLINE=97311416; PubMed=9168133;  
 RA Sugaya K., Sasamura S.-I., Nohata J., Kimura T., Fukagawa T.,  
 Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;  
 "Gene organization of human NOTCH4 and (CTG)n polymorphism in this  
 RT human counterpart gene of mouse proto-oncogene Int3.";  
 RL Gene 189:235-244(1997).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).  
 RC TISSUE=Bone marrow, and Heart;  
 RX MEDLINE=98360091; PubMed=9693032;  
 RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,  
 Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;  
 "Cloning, characterization, and the complete 56.8-kilobase DNA  
 RT sequence of the human NOTCH4 gene.";  
 RL Genomics 51:45-58(1998).  
 [3]  
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.  
 RA Miyagawa T., Tokunaga K., Hojo H.;  
 RT "Human notch4 gene variant.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Miceiadis E., Henrique D., Carcangiu M.-L.,  
 Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;  
 "Human ligands of the Notch receptor.";  
 RL Am. J. Pathol. 154:785-794(1999).  
 -1- FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Delta1 to regulate cell fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-U kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs. May regulate branching morphogenesis in the  
 CC developing vascular system (By similarity).  
 -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing, NICD is translocated to the nucleus.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in  
 CC the lung and placenta and at low levels in the liver, skeletal  
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow  
 CC and fetal liver. No expression was seen in adult brain or  
 CC peripheral blood leukocytes.  
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -1- PTM: Phosphorylated (By similarity).  
 CC -1- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal  
 CC peptide) is polymorphic and the number of Leu varies in the  
 CC population (from 6 to 12).  
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 1438 to 1463.  
 CC  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 CC EMBL; D63395; BAA09708.1; ALT\_FRAME.  
 CC EMBL; D86566; BAA13116.1; -  
 CC EMBL; U95299; AAC32288.1; -  
 CC EMBL; U95335; AAC63097.1; -  
 CC EMBL; AB023361; BAB20317.1; -  
 CC EMBL; AB024520; BAA88951.1; -  
 CC EMBL; AB024578; BAA88952.1; -  
 CC HSSP; P08709; 1BF9.  
 CC GeneW; HGNC:7884; NOTCH4.  
 DR MIM; 164951; -  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 26.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 2.  
 DR PRINTS; PR00010; EGFBLDOD.  
 DR PRINTS; PR00011; EGFAMININ.  
 DR PRINTS; PR00012; FNTYPTI.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_CA; 11.  
 DR SMART; SM00179; EGF\_CA; 11.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 5.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 DR PROSITE; PS00022; EGF\_1; 28.  
 DR PROSITE; PS01186; EGF\_2; 21.  
 DR PROSITE; PS01187; EGF\_CA; 9.  
 DR Receptor; Transcription regulation; Activator; Differentiation;



```

DR Pfam: PF02210; TSPN; 1.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 3.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00210; TSPN; 1.
DR SMART: SM00214; WVC; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS01208; WVC; 2.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 1 24
FT DOMAIN 25 816
FT DOMAIN 30 258
FT DOMAIN 272 331
FT DOMAIN 332 396
FT DOMAIN 397 439
FT DOMAIN 440 481
FT DOMAIN 482 522
FT DOMAIN 521 553
FT DOMAIN 555 601
FT DOMAIN 602 637
FT DOMAIN 638 693
FT DOMAIN 698 756
FT DOMAIN 758 813
FT DOMAIN 813 813
FT DISULFID 401 422
FT DISULFID 422 438
FT DISULFID 438 444
FT DISULFID 444 457
FT DISULFID 457 466
FT DISULFID 466 480
FT DISULFID 480 499
FT DISULFID 499 508
FT DISULFID 510 521
FT DISULFID 521 535
FT DISULFID 535 541
FT DISULFID 541 552
FT DISULFID 552 572
FT DISULFID 572 581
FT DISULFID 581 600
FT DISULFID 600 619
FT DISULFID 619 628
FT DISULFID 628 630
FT DISULFID 630 636
FT CARBOHYD 53 53
FT CARBOHYD 225 225
FT CARBOHYD 293 293
FT CARBOHYD 298 298
FT CARBOHYD 517 517
FT CARBOHYD 615 615
FT CARBOHYD 635 635
SQ SEQUENCE 816 AA; 91163 MW; 5BD0A946F87E74D CRC64;

Query Match 12.2%; Score 184; DB 1; Length 816;
Best Local Similarity 28.8%; Pred. No. 6; 1e-07;
Matches 46; Conservative 22; Mismatches 64; Indels 28; Gaps 7;
QY 26 PGRVCAVRAGHPVSESFQRYVQPELTT---CDGHRACSTRTTYRARRSGLAPA 82
DB 461 PGRVCAVRAGHPVSESFQRYVQPELTT---CDGHRACSTRTTYRARRSGLAPA 82
QY 83 RPRVACCPGKRTSGLPAGCAAIICPPRCNGGSCVQPRCRCPAGMRGDTGQSDVDECS 142
DB 505 GHNCVCCKEYGTN---GTTCKAFCKDGRNGGACIAAVVACPGQFTGSPCEITIDEC 504
QY 143 ARGGGCGQR---CVNTAGSYWCQCEHSHLSADGTLVCPVG 180
DB 561 EGFVQCDSRANCTNLPRWHCECRDGYH---DNGMFAFG 597

```

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AC Q92832; Q9V472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C-binding protein NEHL1 precursor (NEHL-like protein 1)
DE (NEHL-related protein 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97131504; PubMed=8975702;
RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
RT "Cloning and characterization of two novel human cDNAs (NEHL1 and
RT NEHL2) encoding proteins with six EGF-like repeats.";
RL Genomics 38:273-276 (1996).
RN [2]
RP SEQUENCE OF 363-810 FROM N.A.
RA Ting K., Vascariis H., Mulliken J.B., Bertolami C., Wen Z.,
RA Young M., Tieu A., Kwong E.;
RT "Nei homolog gene expression in craniofacial anomalies.";
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1 SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1 DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
CC -1 SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC -1 SIMILARITY: CONTAINS 5 WVC DOMAINS.
CC -1 SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -1 CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITIONS 427 AND 771.
CC
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CC
DR EMBL: D83017; BAA11680.1; -
DR EMBL: U57523; AAB06946.1; ALT_FRAME.
DR HSSP: P07204; 1ADK.
DR Genew: HGNC:7750; NEHL1.
DR MIM: 602319; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF_Like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR003129; TSPN.
DR InterPro: IPR001007; WVC_C.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00093; WVC; 3.
DR Pfam: PF02210; TSPN; 1.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00001; EGF_Like; 4.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00214; WVC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS01208; WVC; 2.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 1 16
FT DOMAIN 81 810
FT DOMAIN 273 331
FT DOMAIN 335 390
FT WVC 1.
FT WVC 2.

```

FT DOMAIN 391 433 EGF-LIKE 1. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 434 475 EGF-LIKE 2.  
 FT DOMAIN 476 516 EGF-LIKE 3.  
 FT DOMAIN 515 547 EGF-LIKE 4.  
 FT DOMAIN 549 595 EGF-LIKE 5. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 596 631 EGF-LIKE 6. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 632 687 WFC 3.  
 FT DOMAIN 692 750 WFC 4.  
 FT DOMAIN 752 807 WFC 5.  
 FT DISULFID 395 407 BY SIMILARITY.  
 FT DISULFID 408 416 BY SIMILARITY.  
 FT DISULFID 418 432 BY SIMILARITY.  
 FT DISULFID 438 451 BY SIMILARITY.  
 FT DISULFID 445 460 BY SIMILARITY.  
 FT DISULFID 462 474 BY SIMILARITY.  
 FT DISULFID 480 493 BY SIMILARITY.  
 FT DISULFID 487 502 BY SIMILARITY.  
 FT DISULFID 504 515 BY SIMILARITY.  
 FT DISULFID 519 529 BY SIMILARITY.  
 FT DISULFID 523 535 BY SIMILARITY.  
 FT DISULFID 537 546 BY SIMILARITY.  
 FT DISULFID 553 566 BY SIMILARITY.  
 FT DISULFID 560 575 BY SIMILARITY.  
 FT DISULFID 577 594 BY SIMILARITY.  
 FT DISULFID 600 613 BY SIMILARITY.  
 FT DISULFID 607 622 BY SIMILARITY.  
 FT DISULFID 624 630 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CONFLICT 383 383 N -> D (IN REF. 2).  
 FT CONFLICT 573 573 Y -> H (IN REF. 2).  
 FT CONFLICT 626 626 S -> C (IN REF. 2).  
 SQ SEQUENCE 810 AA; 89606 MW; 549465EA3F7AEED0 CRC64;  
 Query Match 12.2%; Score 183; DB 1; Length 810;  
 Best Local Similarity 38.5%; Pred. No. 7.3e-07;  
 Matches 37; Conservative 11; Mismatches 36; Indels 10; Gaps 3;  
 QY 88 CPGWKRISGLPGACGAATCQPPCRNGSCVOPRCRCPCAGWRGTCQSDVDECSARRGG 147  
 Db 504 CKPGYVGN---GTICRAFCEGCRGTCVAPNKCVCPSGFTGSHCEKXIDCECSEGTIE 559  
 QY 148 C--PQRCVNTAGSYWCQWEGH---SLGADGTLGV 177  
 Db 560 CHNHSRCVNLPGWYHCECRSGFHDHDTYSLSGESCI 595  
 RESULT 5  
 FN2\_MOUSE STANDARD; PRT; 2907 AA.  
 AC Q61555; Q63957;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 2 precursor.  
 GN FN2 OR FN2-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95263670; PubMed=7744963;

RA Zhang H., Hu W., Ramirez F.;  
 RT "Developmental expression of fibrillin genes suggests heterogeneity  
 RL of extracellular microfibrils";  
 RN J. Cell Biol. 129:1165-1176(1995).  
 RP [2]  
 RX SEQUENCE OF 210-317 FROM N.A.  
 RA MEDLINE=94140368; PubMed=8307578;  
 Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
 Francke U.;  
 RA "Fibrillin genes map to regions of conserved mouse/human synteny on  
 RT mouse chromosomes 2 and 18";  
 RL Genomics 18:667-672(1993).  
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
 CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
 CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
 CC  
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 CC  
 CC  
 DR EMBL; L39790; AAA74908.1; -;  
 DR EMBL; S69359; AAC60685.1; -;  
 DR HSSP; P35855; 1EMN.  
 DR MGD; MGI:95490; Fbn2.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001861; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR002212; Fibrill-assoc.  
 DR Pfam; PF00608; EGF; 46.  
 DR Pfam; PF00683; TB; 9.  
 DR PRINTS; PR00010; EGFELOOD.  
 DR SMART; SM00179; EGF\_CA; 43.  
 DR SMART; SM00001; EGF\_Like; 3.  
 DR PROSITE; PS00010; ASX HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 36.  
 DR PROSITE; PS01187; EGF\_CA; 43.  
 DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 KW Repeat; Signal; Multigene family.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 2907 FIBRILLIN 2.  
 FT DOMAIN 111 142 EGF-LIKE 1.  
 FT DOMAIN 145 176 EGF-LIKE 2.  
 FT DOMAIN 176 208 EGF-LIKE 3.  
 FT DOMAIN 276 317 EGF-LIKE 4. CALCIIUM-BINDING.  
 FT DOMAIN 318 359 EGF-LIKE 5. CALCIIUM-BINDING.  
 FT REPEAT 360 426 TGFBP 1.  
 FT DOMAIN 487 527 EGF-LIKE 6.  
 FT DOMAIN 528 567 EGF-LIKE 7. CALCIIUM-BINDING.  
 FT DOMAIN 568 609 EGF-LIKE 8. CALCIIUM-BINDING.  
 FT DOMAIN 610 650 EGF-LIKE 9. CALCIIUM-BINDING.  
 FT DOMAIN 651 691 EGF-LIKE 10. CALCIIUM-BINDING.  
 FT REPEAT 692 760 TGFBP 2.  
 FT DOMAIN 761 802 EGF-LIKE 11. CALCIIUM-BINDING.  
 FT DOMAIN 803 844 EGF-LIKE 12. CALCIIUM-BINDING.  
 FT DOMAIN 845 883 EGF-LIKE 13. CALCIIUM-BINDING.  
 FT DOMAIN 948 989 EGF-LIKE 14. CALCIIUM-BINDING.  
 FT REPEAT 990 1065 TGFBP 3.  
 FT DOMAIN 1066 1107 EGF-LIKE 15. CALCIIUM-BINDING.  
 FT DOMAIN 1108 1150 EGF-LIKE 16. CALCIIUM-BINDING.  
 FT DOMAIN 1151 1192 EGF-LIKE 17. CALCIIUM-BINDING.  
 FT DOMAIN 1193 1234 EGF-LIKE 18. CALCIIUM-BINDING.  
 FT DOMAIN 1235 1275 EGF-LIKE 19. CALCIIUM-BINDING.  
 FT DOMAIN 1276 1317 EGF-LIKE 20. CALCIIUM-BINDING.  
 FT DOMAIN 1318 1359 EGF-LIKE 21. CALCIIUM-BINDING.  
 FT DOMAIN 1360 1400 EGF-LIKE 22. CALCIIUM-BINDING.

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FT DOMAIN 1401 1441 EGF-LIKE 23, CALCIUM-BINDING.
FT DOMAIN 1442 1483 EGF-LIKE 24, CALCIUM-BINDING.
FT DOMAIN 1484 1524 EGF-LIKE 25, CALCIUM-BINDING.
FT DOMAIN 1525 1565 EGF-LIKE 26, CALCIUM-BINDING.
FT REPEAT 1566 1642 TGFBP 4.
FT DOMAIN 1643 1684 EGF-LIKE 27, CALCIUM-BINDING.
FT DOMAIN 1685 1726 EGF-LIKE 28, CALCIUM-BINDING.
FT REPEAT 1727 1800 TGFBP 5.
FT DOMAIN 1801 1842 EGF-LIKE 29, CALCIUM-BINDING.
FT DOMAIN 1843 1884 EGF-LIKE 30, CALCIUM-BINDING.
FT DOMAIN 1885 1926 EGF-LIKE 31, CALCIUM-BINDING.
FT DOMAIN 1927 1965 EGF-LIKE 32, CALCIUM-BINDING.
FT DOMAIN 1966 2008 EGF-LIKE 33, CALCIUM-BINDING.
FT DOMAIN 2009 2048 EGF-LIKE 34, CALCIUM-BINDING.
FT DOMAIN 2049 2090 EGF-LIKE 35, CALCIUM-BINDING.
FT REPEAT 2091 2163 TGFBP 6.
FT DOMAIN 2164 2205 EGF-LIKE 36, CALCIUM-BINDING.
FT DOMAIN 2206 2245 EGF-LIKE 37, CALCIUM-BINDING.
FT DOMAIN 2246 2286 EGF-LIKE 38, CALCIUM-BINDING.
FT DOMAIN 2287 2330 EGF-LIKE 39, CALCIUM-BINDING.
FT DOMAIN 2331 2372 EGF-LIKE 40, CALCIUM-BINDING.
FT REPEAT 2373 2441 TGFBP 7.
FT DOMAIN 2442 2483 EGF-LIKE 41, CALCIUM-BINDING.
FT DOMAIN 2484 2524 EGF-LIKE 42, CALCIUM-BINDING.
FT DOMAIN 2525 2563 EGF-LIKE 43, CALCIUM-BINDING.
FT DOMAIN 2564 2606 EGF-LIKE 44, CALCIUM-BINDING.
FT DOMAIN 2607 2646 EGF-LIKE 45, CALCIUM-BINDING.
FT DOMAIN 2647 2687 EGF-LIKE 46, CALCIUM-BINDING.
FT DOMAIN 2688 2727 EGF-LIKE 47, CALCIUM-BINDING.
FT DISULFID 115 124 BY SIMILARITY.
FT DISULFID 119 130 BY SIMILARITY.
FT DISULFID 132 141 BY SIMILARITY.
FT DISULFID 149 159 BY SIMILARITY.
FT DISULFID 153 164 BY SIMILARITY.
FT DISULFID 166 175 BY SIMILARITY.
FT DISULFID 180 190 BY SIMILARITY.
FT DISULFID 184 196 BY SIMILARITY.
FT DISULFID 198 207 BY SIMILARITY.
FT DISULFID 280 292 BY SIMILARITY.
FT DISULFID 287 301 BY SIMILARITY.
FT DISULFID 303 316 BY SIMILARITY.
FT DISULFID 322 334 BY SIMILARITY.
FT DISULFID 329 343 BY SIMILARITY.
FT DISULFID 345 358 BY SIMILARITY.
FT DISULFID 491 503 BY SIMILARITY.
FT DISULFID 498 512 BY SIMILARITY.
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 532 542 BY SIMILARITY.
FT DISULFID 537 551 BY SIMILARITY.
FT DISULFID 553 566 BY SIMILARITY.
FT DISULFID 572 584 BY SIMILARITY.
FT DISULFID 579 593 BY SIMILARITY.
FT DISULFID 595 608 BY SIMILARITY.
FT DISULFID 614 625 BY SIMILARITY.
FT DISULFID 620 634 BY SIMILARITY.
FT DISULFID 636 649 BY SIMILARITY.
FT DISULFID 655 666 BY SIMILARITY.
FT DISULFID 661 675 BY SIMILARITY.
FT DISULFID 677 690 BY SIMILARITY.
FT DISULFID 765 777 BY SIMILARITY.
FT DISULFID 772 786 BY SIMILARITY.
FT DISULFID 788 801 BY SIMILARITY.
FT DISULFID 807 819 BY SIMILARITY.
FT DISULFID 814 828 BY SIMILARITY.
FT DISULFID 830 843 BY SIMILARITY.
FT DISULFID 849 859 BY SIMILARITY.
FT DISULFID 868 883 BY SIMILARITY.
FT DISULFID 870 883 BY SIMILARITY.
FT DISULFID 952 964 BY SIMILARITY.
FT DISULFID 956 973 BY SIMILARITY.
FT DISULFID 975 988 BY SIMILARITY.
FT DISULFID 1070 1082 BY SIMILARITY.
FT DISULFID 1077 1091 BY SIMILARITY.

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FT DISULFID 1093 1106 BY SIMILARITY.
FT DISULFID 1112 1124 BY SIMILARITY.
FT DISULFID 1119 1133 BY SIMILARITY.
FT DISULFID 1135 1149 BY SIMILARITY.
FT DISULFID 1155 1167 BY SIMILARITY.
FT DISULFID 1162 1176 BY SIMILARITY.
FT DISULFID 1178 1191 BY SIMILARITY.
FT DISULFID 1197 1209 BY SIMILARITY.
FT DISULFID 1204 1218 BY SIMILARITY.
FT DISULFID 1220 1233 BY SIMILARITY.
FT DISULFID 1239 1250 BY SIMILARITY.
FT DISULFID 1246 1259 BY SIMILARITY.
FT DISULFID 1261 1274 BY SIMILARITY.
FT DISULFID 1280 1292 BY SIMILARITY.
FT DISULFID 1287 1301 BY SIMILARITY.
FT DISULFID 1303 1316 BY SIMILARITY.
FT DISULFID 1322 1334 BY SIMILARITY.
FT DISULFID 1329 1343 BY SIMILARITY.
FT DISULFID 1345 1358 BY SIMILARITY.
FT DISULFID 1364 1377 BY SIMILARITY.
FT DISULFID 1371 1386 BY SIMILARITY.
FT DISULFID 1388 1399 BY SIMILARITY.
FT DISULFID 1405 1418 BY SIMILARITY.
FT DISULFID 1412 1427 BY SIMILARITY.
FT DISULFID 1429 1440 BY SIMILARITY.
FT DISULFID 1446 1458 BY SIMILARITY.
FT DISULFID 1453 1467 BY SIMILARITY.
FT DISULFID 1469 1482 BY SIMILARITY.
FT DISULFID 1488 1499 BY SIMILARITY.
FT DISULFID 1494 1508 BY SIMILARITY.
FT DISULFID 1510 1523 BY SIMILARITY.
FT DISULFID 1529 1540 BY SIMILARITY.
FT DISULFID 1535 1549 BY SIMILARITY.
FT DISULFID 1551 1564 BY SIMILARITY.
FT DISULFID 1647 1659 BY SIMILARITY.
FT DISULFID 1654 1668 BY SIMILARITY.
FT DISULFID 1670 1683 BY SIMILARITY.
FT DISULFID 1689 1701 BY SIMILARITY.
FT DISULFID 1696 1710 BY SIMILARITY.
FT DISULFID 1712 1725 BY SIMILARITY.

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Query Match 12.1%, Score 182.5, DB 1, Length 2907;  
 Best Local Similarity 23.5%, Pred. No. 2.8e-06;  
 Matches 59; Conservative 20; Mismatches 85; Indels 87; Gaps 7;

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QY 2 RGSQEVLMWLVAVGTEHAY-----RGRVCAVRAHGDVSPVQRYQPLT 54
Db 77 RQQETLRG---PNVCGSRFHSYCCPGMKTLPGNGQICVPICRNSCGGDFCSR---PNWC 130
QY 55 TCDGRACST--YRTIYTVAYRSPGLAPARPRVACCPGMRKTSGLPGACGAICQPPCR 112
Db 131 TCSGQISPTCCRKSIQCCSVRCNMNGCTCADDHCCQCGIYGT-----YCCQPVCENCQ 185
QY 113 NGSCVQPRCRCPAGMTGDTQ----- 135
Db 186 NGRCICGPRCVCVYFGTGPCERDYRTGCFYVNNOMCGQLTGLVCTKTLCAITGR 245
QY 136 -----SDVDECSARGGCP-QRCNTAGSYWCQWE 165
Db 246 AMGHRCMCPAPQPCRCRPFIPNRTGACQDVDECAIPGLCGGNCINTVSGSECRCPA 305
QY 166 GHSLSADGTLQ 176
Db 306 GHKQSETTQKC 316

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RESULT 6  
 NEL2\_HUMAN  
 ID NEL2\_HUMAN STANDARD; PRT; 816 AA.  
 AC Q99435;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)



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CC EMBL: U48246; AAC72252.1; -

DR HSSP; P35555; IEDM.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001791; laminin\_G.

DR InterPro; IPR003129; TSPN.

DR InterPro; IPR001007; VWF\_C.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00093; WVC; 3.

DR Pfam; PF02210; TSPN; 1.

DR SMART; SM00179; EGF\_CA; 2.

DR SMART; SM00001; EGF\_Like; 4.

DR SMART; SM00282; LamG; 1.

DR SMART; SM00214; TSPN; 1.

DR SMART; SM00214; VMC; 4.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 3.

DR PROSITE; PS01187; EGF\_CA; 3.

DR PROSITE; PS01208; WVC; 2.

DR Glycoprotein; EGF-Like domain; Repeat; Signal.

KT SIGNAL 1 16

KT CHAIN 17 810

KT DOMAIN 81 230

KT DOMAIN 273 331

KT DOMAIN 335 390

KT DOMAIN 391 433

KT DOMAIN 434 475

KT DOMAIN 476 516

KT DOMAIN 515 547

KT DOMAIN 549 595

KT DOMAIN 596 631

KT DOMAIN 632 687

KT DOMAIN 692 750

KT DOMAIN 752 807

KT DISULFID 395 407

KT DISULFID 401 416

KT DISULFID 418 432

KT DISULFID 438 451

KT DISULFID 445 460

KT DISULFID 462 474

KT DISULFID 480 493

KT DISULFID 487 502

KT DISULFID 504 515

KT DISULFID 519 529

KT DISULFID 523 535

KT DISULFID 537 546

KT DISULFID 553 566

KT DISULFID 560 575

KT DISULFID 577 594

KT DISULFID 600 613

KT DISULFID 607 622

KT DISULFID 624 630

KT CARBOHYD 53 53

KT CARBOHYD 83 83

KT CARBOHYD 224 224

KT CARBOHYD 294 294

KT CARBOHYD 372 372

KT CARBOHYD 511 511

KT CARBOHYD 562 562

KT CARBOHYD 609 609

KT CARBOHYD 708 708

KT SEQUENCE 810 AA; 89212 MW; 46F09C46A9A9A0B C6C64;

Query Match 12.0%; Score 181; DB 1; Length 810;

Best Local Similarity 37.5%; Pred. No. 1e-06;  
 Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 88 CCGKMTSLPACGALICQPCPCNGSCVDPGRCPAGMRGDTQSGDVDCSARRG 147

DB 504 CQGVYON-----GLTKAFEEBCRGYGTCAVANKVCPSGFGSGCEKIDBCAGFVE 559

QY 148 CP--ORCVNTAGSYWCQWEGH-----SLSADGTLGV 177

DB 560 CHNYSRCVNLPGWYHCECRSGFRHDDGTYSLSGSCT 595

RESULT 8

NEL2\_NEL

ID ID

AC 062918; STANDARD; PRT; 816 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Protein kinase C-binding protein NEL2 precursor (NEL-like protein 2).

OS NEL2 OR NEL.

GN Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=20017976; PubMed=10548494;

RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,

RA Abe T., Matsubashi S., Ting K.;

RT "Biochemical characterization and expression analysis of neural

RT chromospondin-1-like proteins NEL1 and NEL2.";

RL Biochem. Biophys. Res. Commun. 265:79-86 (1999).

RN [2]

RP TSP N-TERMINAL DOMAIN.

RX MEDLINE=98153258; PubMed=9480764;

RA Beckmann G., Hanke J., Bork P., Reich J.;

RT "Merging extracellular domains: fold prediction for laminin G-like

RT and amino-terminal thrombospondin-like modules based on homology to

RT pentraxins.";

RL J. Mol. Biol. 275:725-730 (1998).

CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.

CC -1-SUBCELLULAR LOCATION: Secreted.

CC -1-SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.

CC -1-SIMILARITY: CONTAINS 5 WVC DOMAINS.

CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL: U48245; AAC72245.1; -

DR HSSP; P00740; IEDM.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001791; laminin\_G.

DR InterPro; IPR003129; TSPN.

DR InterPro; IPR001007; VWF\_C.

DR Pfam; PF00008; EGF; 5.

DR Pfam; PF00093; WVC; 3.

DR Pfam; PF02210; TSPN; 1.

DR SMART; SM00179; EGF\_CA; 3.

DR SMART; SM00001; EGF\_Like; 3.

DR SMART; SM00282; LamG; 1.

DR SMART; SM00214; TSPN; 1.

DR SMART; SM00214; VMC; 3.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.

DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; WFEC; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 816  
 FT DOMAIN 30 258  
 FT DOMAIN 272 331  
 FT DOMAIN 332 396  
 FT DOMAIN 397 439  
 FT DOMAIN 440 481  
 FT DOMAIN 482 522  
 FT DOMAIN 521 553  
 FT DOMAIN 555 601  
 FT DOMAIN 602 637  
 FT DOMAIN 638 693  
 FT DOMAIN 698 756  
 FT DOMAIN 758 813  
 FT DISULFID 401 413  
 FT DISULFID 407 422  
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 FT DISULFID 486 499  
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 FT DISULFID 510 521  
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 FT DISULFID 529 541  
 FT DISULFID 543 552  
 FT DISULFID 559 572  
 FT DISULFID 566 581  
 FT DISULFID 583 600  
 FT DISULFID 606 619  
 FT DISULFID 613 628  
 FT DISULFID 630 636  
 FT CARBOHYD 53 53  
 FT CARBOHYD 225 225  
 FT CARBOHYD 293 293  
 FT CARBOHYD 298 298  
 FT CARBOHYD 517 517  
 FT CARBOHYD 615 615  
 FT CARBOHYD 635 635  
 SQ SEQUENCE 816 AA; 90952 MW; A99976078060D6B CRC64;  
 Query Match 11.9%; Score 179.5; DB 1; Length 816;  
 Best Local Similarity 35.8%; Pred. No. 1.4e-06;  
 Matches 34; Conservative 15; Mismatches 37; Indels 9; Gaps 3;  
 QY 88 CPGKWKRTSGLPACGAALCQPCRNNGSCVQPGRCPCAGWRGUTCSVDVDCSARRGG 147  
 Db 510 CKPGYGTGN---GTTCKAFCKDCKNGGACIAAANVCACPGQFTGPGSCETIDECSEGFVQ 565  
 QY 148 CQQR--CVNTAGSYWCQCEHSLGSDGTLVCPKG 180  
 Db 566 CDSRANCINLPWYHCECRDGYH---DNGWFAPGG 597  
 RESULT 9  
 ID CD93\_HUMAN STANDARD; PRT; 652 AA.  
 AC Q9NPY3; O00274;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement component C1q receptor precursor (Complement component 1, q  
 DE subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)  
 DE (CD93 antigen) (CDw93).  
 OS Homo sapiens (Human).  
 GN C1QR1 OR CD93.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX PubMed=9047234;  
 RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;  
 RT "cDNA cloning and primary structure analysis of C1qR(p), the human  
 C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";  
 RL Immunity 6:119-129(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT ALA-318.  
 RX PubMed=11781389;  
 RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,  
 Prager E., Saffler G., Madic O., Stockinger H., Knapp W.;  
 RT "Identification of human CD93 as the phagocytic C1q receptor (C1qR(p))  
 by expression cloning.";  
 RL J. Leukoc. Biol. 71:133-140(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,  
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 Levasiaiko M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,  
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,  
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Leukocyte;  
 RA Strausberg R.;  
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP CHARACTERIZATION.  
 RX PubMed=11994479;  
 RA McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.;  
 RT "Human C1qR(p) is identical with CD93 and the mN1-11 antigen but does  
 not bind C1q.";  
 RL J. Immunol. 168:5222-5232(2002).  
 RN [6]  
 RP O-GLYCOSYLATION.  
 RX PubMed=10092817;  
 RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;  
 RT "C1qR(p) is a heavily O-glycosylated cell surface protein involved in  
 the regulation of phagocytic activity.";  
 RL J. Immunol. 162:3583-3589(1999).  
 CC -1- FUNCTION: Receptor (or element of a larger receptor complex) for  
 C1q, mannose-binding lectin (MBL2) and pulmonary surfactant  
 protein A (SPA). May mediate the enhancement of phagocytosis in  
 monocytes and macrophages upon interaction with soluble defense  
 collagens. May play a role in intercellular adhesion.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,  
 platelets, cells of myeloid origin, such as monocytes and





RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
[4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Oregon-R;  
RC MEDLINE=20196011; PubMed=10731137;  
RX Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,  
RA Dreano S., Gloux S., Leleau V., Mottier S., Galibert F., Borkova D.,  
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,  
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,  
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,  
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,  
RA Callister D.M., Campbell L.A., Darlamsou A., Henderson N.S.,  
RA McWilliam P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
RA Glover D.M.;  
RT "From sequence to chromosome: the tip of the X chromosome of *D. melanogaster*,"  
RN Science 287:2220-2222(2000).  
[5]  
RP SEQUENCE OF 2505-2611 FROM N.A.  
RX MEDLINE=85099329; PubMed=2981631;  
RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;  
RT "opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in *D. melanogaster*,"  
RL Cell 40:55-62(1985).  
[6]  
RN SEQUENCE OF 1-8 FROM N.A.  
RX MEDLINE=87257846; PubMed=3037327;  
RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;  
RT "Restriction of P-element insertions at the Notch locus of *Drosophila melanogaster*,"  
RL Mol. Cell. Biol. 7:1545-1548(1987).  
[7]  
RP REVIEW.  
RA Harris W.A.;  
RT "Many cell types specified by Notch function,";  
RL Curr. Biol. 1:120-122(1991).  
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with Su(H) (Suppressor of hairless) and activates genes of the enhancer of split locus. Essential for proper differentiation of ectoderm.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.

CC -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
CC -!- SIMILARITY: CONTAINS 6 ANK REPEATS.  
-----  
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-----  
CC EMBL; M16152; AAB59220.1; -  
CC EMBL; M16153; AAB59220.1; JOINED.  
CC EMBL; M16149; AAB59220.1; JOINED.  
CC EMBL; M16150; AAB59220.1; JOINED.  
CC EMBL; M16151; AAB59220.1; JOINED.  
CC EMBL; M03508; AAA28725.1; -  
CC EMBL; M13689; AAA28725.1; JOINED.  
CC EMBL; K03507; AAA28725.1; JOINED.  
CC EMBL; AE003426; AAF45848.2; -  
CC EMBL; AL035436; CAB37610.1; -  
CC EMBL; AL035395; CAB37610.1; JOINED.  
CC EMBL; M12175; AAA74496.1; -  
CC EMBL; M16025; AAA28726.1; -  
CC PIR; A24420; A24420.  
CC PIR; A24768; A24768.  
CC PIR; A05267; A05267.  
CC HSSP; P00740; 1EDM.  
CC FlyBase; FBgn004647; N.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000152; Asx\_hydroxyl.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR000742; EGF\_2.  
CC InterPro; IPR001881; EGF\_Ca.  
CC InterPro; IPR001438; EGF\_II.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR000800; Notch.  
CC Pfam; PF00008; EGF; 36.  
CC Pfam; PF00023; ank; 6.  
CC PRINTS; PR00010; EGFBLD.  
CC PRINTS; PR00011; EGFLAMININ.  
CC PRINTS; PR01452; NOTCH.  
CC SMART; SM00248; ANK; 7.  
CC SMART; SM00181; EGF; 36.  
CC SMART; SM00179; EGF\_CA; 35.  
CC SMART; SM00004; NL; 2.  
CC PROSITE; PS50088; ANK\_REPEAT; 5.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS00010; ASX\_HYDROXYL; 22.  
CC PROSITE; PS00022; EGF\_1; 34.  
CC PROSITE; PS01186; EGF\_2; 28.  
CC PROSITE; PS01187; EGF\_CA; 21.  
KW Receptor; Transcription regulation; Activator; Differentiation;  
KW Developmental protein; Neurogenesis; Repeat; ANK repeat;  
KW EGF-like domain; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 44  
FT CHAIN 45 2703  
FT DOMAIN 45 1745  
FT TRANSMEM 1746 1766  
FT DOMAIN 1767 2703  
FT DOMAIN 58 95  
FT DOMAIN 96 136  
FT DOMAIN 139 176  
FT DOMAIN 177 215  
FT DOMAIN 217 253  
FT DOMAIN 255 291  
FT DOMAIN 293 329  
FT DOMAIN 331 370  
FT DOMAIN 372 408  
FT DOMAIN 409 447  
FT DOMAIN 449 486

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FT DOMAIN 488 524 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 526 562 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 564 600 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 602 637 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 639 675 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 677 713 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 715 751 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 753 789 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 791 827 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 829 865 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 867 905 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 907 944 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).

Query Match 11.7%; Score 176; DB 1; Length 2703;
Best Local Similarity 25.8%; Pred. No. 8.3e-06;
Matches 58; Conservative 21; Mismatches 62; Indels 84; Gaps 13;

QY 18 GGEHAYRPGRRACVAVRAH--GDPVSESFYQRYVPFLITTCDSHRACSYRT---IYRT 71
DB 70 GGCVCVQLNGKTYCACDSHYVD-----YCEHRNPNCSMRCONGSTCQV 113
QY 72 AYRRSPGLAPRRRYAC-CP-GWKRT---SGLPGACGAAIC----- 107
DB 114 TFRN-----GRGISCKCPGLGFDESLCEIAYNACDHYTCLNGSTCQKLTLEYTCACA 167
QY 108 -----QPPCNSSCV-----QPRCRCPAGRGDTQSDVDECSA--R 144
DB 168 NGYTCRCETKNLCASSPCRNATCTALAGSSFTCSCPFGTDCSYDIEBCQNPCK 227
QY 145 RGGCPRCVNTAGSYWQCQWEGHSLADGTLCPKGGPRVAVNP 189
DB 228 YGG---TCVNTGSHSYQCMCPGTYT---GKDCDXTKYP--CSPSP 263

RESULT 11
NEL_CHICK STANDARD; PRT; 816 AA.
AC 090827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NEL protein precursor (93 kDa protein).
OS NEL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=95383734; PubMed=7655083;
RA Matsubashi S., Noji S., Koyama E., Myokai F., Ohuchi H.,
RA Taniguchi S., Horii K.;
RT "New gene, nel, encoding a M(r) 93 K protein with EGF-like repeats is
RT strongly expressed in neural tissues of early stage chick embryos.";
RL Dev. Dyn. 203:212-222(1995).
RN [2]
RP TSP N-TERMINAL DOMAIN.
RA MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RL J. Mol. Biol. 275:725-730(1998).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EARLY EMBRYONIC NEURAL
CC TISSUES (BRAIN, SPINAL CORD, DORSAL ROOT GANGLION), LESS IN OTHER
CC TISSUES SUCH AS CELLS AROUND CARTILAGE, MYOCARDIUM, LUNG
CC MESENCHYMAL CELLS, AND LIVER. AFTER HATCHING EXPRESSION IS
CC RESTRICTED TO NEURAL TISSUES INCLUDING RETINA.
CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 WMFC DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

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CC -----
CC EMBL; D86747; BAA13167.1; -.
CC HSSP; P00740; 1EDM.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000561; EGF-Like.
CC InterPro; IPR001881; EGF-Ca.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR003129; TSPN.
CC InterPro; IPR001007; WMF_C.
CC Pfam; PF00008; EGF; 5.
CC Pfam; PF00093; WWC; 3.
CC Pfam; PF02210; TSPN; 1.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00001; EGF_Like; 4.
CC SMART; SM00282; LamG; 1.
CC SMART; SM00210; TSPN; 1.
CC SMART; SM00214; WWC; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 4.
CC PROSITE; PS01187; EGF_CA; 3.
CC PROSITE; PS01208; WMFC; 2.
CC Glycoprotein; EGF-like domain; Repeat; Signal.
CC SIGNAL 1 24
CC CHAIN 25 816
CC FT DOMAIN 25 816 NEL PROTEIN.
CC FT DOMAIN 30 258 TSP N-TERMINAL.
CC FT DOMAIN 272 331 WMFC 1.
CC FT DOMAIN 332 396 WMFC 2.
CC FT DOMAIN 397 439 EGF-LIKE 1.
CC FT DOMAIN 440 481 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 482 522 EGF-LIKE 3.
CC FT DOMAIN 521 553 EGF-LIKE 4.
CC FT DOMAIN 555 601 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 602 637 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 638 693 WMFC 3.
CC FT DOMAIN 698 756 WMFC 4.
CC FT DOMAIN 758 813 WMFC 5.
CC FT DOMAIN 401 413 BY SIMILARITY.
CC FT DISULFID 407 422 BY SIMILARITY.
CC FT DISULFID 424 428 BY SIMILARITY.
CC FT DISULFID 444 457 BY SIMILARITY.
CC FT DISULFID 451 466 BY SIMILARITY.
CC FT DISULFID 468 480 BY SIMILARITY.
CC FT DISULFID 486 499 BY SIMILARITY.
CC FT DISULFID 493 508 BY SIMILARITY.
CC FT DISULFID 510 521 BY SIMILARITY.
CC FT DISULFID 525 535 BY SIMILARITY.
CC FT DISULFID 529 541 BY SIMILARITY.
CC FT DISULFID 543 552 BY SIMILARITY.
CC FT DISULFID 559 572 BY SIMILARITY.
CC FT DISULFID 566 581 BY SIMILARITY.
CC FT DISULFID 583 600 BY SIMILARITY.
CC FT DISULFID 606 619 BY SIMILARITY.
CC FT DISULFID 613 628 BY SIMILARITY.
CC FT DISULFID 630 636 BY SIMILARITY.
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 225 225 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 298 298 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 517 517 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 615 615 N-LINKED (GLCNAC; .) (POTENTIAL).
CC FT CARBOHYD 635 635 N-LINKED (GLCNAC; .) (POTENTIAL).
CC SEQUENCE 816 AA; 90968 MW; BPCD8C983C02F831 CRC64;
Query Match 11.7%; Score 175.5; DB 1; Length 816;

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Best Local Similarity 38.6%; Pred. No. 2.8e-06;  
 Matches 32; Conservative 13; Mismatches 33; Indels 5; Gaps 2;

QY 100 GACGAAICQPPCRNGGSCVQVGRGCRCPAGWGRDTCQSDVDECSARRGGCPOR--CVNTAG 157  
 DB 518 GTVCKAFKDCGRNGGAGTASNVACAPQGGFTGPGSCETIDECSDGFGVQCDSRANCINLPG 577

QY 158 SYWCOCWEGHSLSADGTLCPVKG 180  
 DB 578 WYHCECRDGYH---DNGWFPSPG 597

RESULT 12

ID\_FBN1\_HUMAN STANDARD; PRT; 2871 AA.

AC P35555;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBN1 OR FBN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=93372860; PubMed=8364578;  
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,  
 RA Pangilinan T., Bonadio J.;  
 RA "Genomic organization of the sequence coding for fibrillin, the  
 RT defective gene product in Marfan syndrome.";  
 RL Hum. Mol. Genet. 2:961-968 (1993).  
 RN [2]  
 RP SEQUENCE OF 1-932 FROM N.A.  
 RC TISSUE=Placenta, and Fibroblast;  
 RX MEDLINE=94010947; PubMed=7691719;  
 RA Corson G.M., Chabberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;  
 RT "Fibrillin binds calcium and is coded by cDNAs that reveal a  
 RT multidomain structure and alternatively spliced exons at the 5'  
 end.";  
 RL Genomics 17:476-484 (1993).  
 RN [3]  
 RP SEQUENCE OF 899-2871 FROM N.A.  
 RX MEDLINE=91304568; PubMed=1852207;  
 RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;  
 RT "Partial sequence of a candidate gene for the Marfan syndrome.";  
 RL Nature 352:334-337 (1991).  
 RN [4]  
 RP SEQUENCE OF 813-1313 FROM N.A.  
 RX MEDLINE=91304567; PubMed=1852206;  
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,  
 RA Tsiouras P., Ramirez F., Hollister D.W.;  
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to  
 RT two different fibrillin genes.";  
 RL Nature 352:330-334 (1991).  
 RN [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE=91317849; PubMed=1860873;  
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;  
 RT "Purification and partial characterization of fibrillin, a cysteine-  
 RT rich structural component of connective tissue microfibrils.";  
 RL J. Biol. Chem. 266:14763-14770 (1991).  
 RN [6]  
 RP STRUCTURE BY NMR OF 2054-2125.  
 RX MEDLINE=98031893; PubMed=9362480;  
 RA Yuan X., Downing A.K., Knott V., Handford P.A.;  
 RT "Solution structure of the transforming growth factor beta-binding  
 RT protein-like module, a domain associated with matrix fibrils.";  
 RL EMBO J. 16:6659-6666 (1997).  
 RN [7]  
 RP STRUCTURE BY NMR OF 2124-2205.

RX MEDLINE=96144829; PubMed=8568869;  
 RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;  
 RT "Calcium binding properties of an epidermal growth factor-like domain  
 RL from human fibrillin-1.";  
 RN [8]  
 RP STRUCTURE BY NMR OF 2124-2205.  
 RX MEDLINE=96222301; PubMed=8653794;  
 RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,  
 RA Handford P.A.;  
 RT "Solution structure of a pair of calcium-binding epidermal growth  
 RT factor-like domains: implications for the Marfan syndrome and other  
 RT genetic disorders.";  
 RL Cell 85:597-605 (1996).  
 RN [9]  
 RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=96174615; PubMed=8594563;  
 RA Colliod G., Beroud C., Soussi T., Junien C., Boileau C.;  
 RT "Software and database for the analysis of mutations in the human  
 RT FBN1 gene.";  
 RL Nucleic Acids Res. 24:137-141 (1996).  
 RN [10]  
 RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=97169383; PubMed=9016526;  
 RA Colliod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,  
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,  
 RA Richards R.I., Wang W., Junien C., Boileau C.;  
 RT "Marfan Database (second edition): software and database for the  
 RT analysis of mutations in the human FBN1 gene.";  
 RL Nucleic Acids Res. 25:147-150 (1997).  
 RN [11]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=98062175; PubMed=9401003;  
 RA Hayward C., Brock D.J.H.;  
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1  
 RT fibrillinopathies.";  
 RL Hum. Mutat. 10:415-423 (1997).  
 RN [12]  
 RP VARIANT MFS PRO-1137.  
 RX MEDLINE=91304569; PubMed=1852208;  
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,  
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,  
 RA Currstin S.M., Stetten G., Meyers D.A., Francomano C.A.;  
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in  
 RT the fibrillin gene.";  
 RL Nature 352:337-339 (1991).  
 RN [13]  
 RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.  
 RX MEDLINE=93250834; PubMed=1301946;  
 RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;  
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome  
 RT patients at cysteine residues in EGF-like domains.";  
 RL Hum. Mutat. 1:366-374 (1992).  
 RN [14]  
 RP VARIANT MFS SER-2307.  
 RX MEDLINE=92235290; PubMed=1569206;  
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,  
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;  
 RT "Marfan phenotype variability in a family segregating a missense  
 RT mutation in the epidermal growth factor-like motif of the fibrillin  
 RT gene.";  
 RL J. Clin. Invest. 89:1674-1680 (1992).  
 RN [15]  
 RP VARIANTS MFS ILE-548 AND ALA-723.  
 RX MEDLINE=94010946; PubMed=8406497;  
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chabberg S.C.,  
 RA Pyeritz R.E., Francomano C.A.;  
 RT "Four novel FBN1 mutations: significance for mutant transcript level  
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan  
 RL syndrome.";  
 RN [16]  
 RP VARIANTS MFS SER-2144.

RA MEDLINE=93278402; PubMed=8504310;  
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;  
 RT "A novel fibrillin mutation in the Marfan syndrome which could  
 RT disrupt calcium binding of the epidermal growth factor-like module,"  
 RL Hum. Mol. Genet. 2:475-477(1993).  
 RN [17]  
 RP VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.  
 RX MEDLINE=9410843; PubMed=8281141;  
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,  
 RA Berg M.A., Miller D.C., Francke U.;  
 RT "Mutation screening of complete fibrillin-1 coding sequence: report  
 RT of five new mutations, including two in 8-cysteine domains,"  
 RL Hum. Mol. Genet. 2:1813-1821(1993).  
 RN [18]  
 RP VARIANTS MFS GLY-217 AND ARG-2627.  
 RX MEDLINE=95067970; PubMed=7977366;  
 RA Karttunen L., Raghunath M., Lonnqvist L., Peltonen L.;  
 RT "A compound-heterozygous Marfan patient: two defective fibrillin  
 RT alleles result in a lethal phenotype,"  
 RL Am. J. Hum. Genet. 55:1083-1091(1994).  
 RN [19]  
 RP VARIANT EL LYS-2447.  
 RX MEDLINE=94245249; PubMed=8188302;  
 RA Lonnqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,  
 RA Peltonen L.;  
 RT "A novel mutation of the fibrillin gene causing ectopia lentis,"  
 RL Genomics 19:573-576(1994).  
 RN [20]  
 RP VARIANT MFS CYS-627.  
 RX MEDLINE=94272487; PubMed=8004112;  
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;  
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains  
 RT of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan  
 RT syndrome patients,"  
 RL Hum. Mol. Genet. 3:373-375(1994).  
 RN [21]  
 RP VARIANT MFS CYS-122.  
 RX MEDLINE=94314977; PubMed=8040326;  
 RA Stahl-Hallengren C., Ukonen T., Kainulainen K., Kristoferson U.,  
 RA Saxne T., Tornqvist K., Peltonen L.;  
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth  
 RT factor-like motifs of the FBN1 polypeptide is connected to a novel  
 RT variant of Marfan syndrome,"  
 RL J. Clin. Invest. 94:709-713(1994).  
 RN [22]  
 RP VARIANT MFS TYR-1223.  
 RX MEDLINE=94351682; PubMed=8071963;  
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;  
 RT "A new missense mutation of fibrillin in a patient with Marfan  
 RT syndrome,"  
 RL J. Med. Genet. 31:338-339(1994).  
 RN [23]  
 RP VARIANT MFS HIS-1170.  
 RX MEDLINE=9514777; PubMed=7870075;  
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;  
 RT "A novel mutation in the fibrillin gene (FBN1) in familial  
 RT arachnoidactyly,"  
 RL Mol. Cell. Probes 8:325-327(1994).  
 RN [24]  
 RP VARIANTS MFS G-217, N-1023; R-1074; Y-1242; R-1513; E-2127; W-2151;  
 RP K-2447 AND R-2511.  
 RX MEDLINE=94184368; PubMed=8136837;  
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;  
 RT "Mutations in the fibrillin gene responsible for dominant ectopia  
 RT lentis and neonatal Marfan syndrome,"  
 RL Nat. Genet. 6:64-69(1994).  
 RN [25]  
 RP VARIANT SER-1127.

Query Match 11.7%; Score 175.5; DB 1; Length 2871;  
 Best Local Similarity 18.9%; Pred. No. 9.6e-06;  
 Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;

QY 75 RSPGLAPRPARYACCPGKMTSGLPQA----- 101  
 DB 54 KGPVCGSRVYNAVCCPGKMT---LPGNQICTVPCRHSCGDPGFCSPNMTCTCPGSGQIAPS 110  
 QY 102 -----CGAICQPPRCNGSSCYQPRGRCPA 127  
 DB 111 CGSRBIQHCHIRKWNNGSSCSDDHCLCQKGYIGTHCGQVPBSSGGLNGRCVAPNRCACTY 170  
 QY 128 GMRGDTCC----- 135  
 DB 171 GFTGQGERDVRHTGCFIVINQMGQGLSGIVCTKQLCATVGRAMGHPCMGCPAOPHP 230  
 QY 136 -----SDVDECGARRGCGP-QRCVNTAGSYWCQCEGHSLSADGTLCTC----- 176  
 DB 231 CRGFIPIRITGACQDVDECOAIPGLCGGNCINVTGSGFECKCPAGHKLTNEVSQCEDID 290  
 QY 177 -----VPKGS-----PPRYANPFG 191  
 DB 291 ECSTIPGICEGGCTNTVSSYPCKCPGPGFTYSPDG 325

## RESULT 13

NTC3 HUMAN

ID NTC3 HUMAN STANDARD; PRT; 2321 AA.

AC Q9DM47; Q9Y6L8; Q9UPL3; Q9UEB3;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neogenetic locus notch homolog protein 3 precursor (Notch 3).  
 GN NTC3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 OX [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=878478; PubMed=8878478;  
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,  
 RA Alomowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J.,  
 RA Vayssières C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,  
 RA Bach J.-F., Bousser M.-G., Tournier-Lasserre E.;  
 RT "Notch3 mutations in CADASIL, a hereditary adult-onset condition  
 RT causing stroke and dementia,"  
 RL Nature 383:707-710(1996).  
 RN [2]

RP SEQUENCE FROM N.A.

RA Gunel M., Aravanis-Tsakonas S.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.

RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Sliwage S.,  
 RA Phan H., Velasco N., Garness J., Dangnan L., Poundstone P.,  
 RA Christensen M., Georgescu A., Avila J., Liu S., Altix C., Andreise T.,  
 RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
 RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,  
 RA Montgomey M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,  
 RA Carrano A.V.;  
 RT "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in  
 RT 19p13.1,"  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]

RP VARIANTS CADASIL Y-49; C-71; C-90; C-110; C-133; C-141; R-146; C-153;  
 RP C-169; C-171; C-182; R-185; S-212; G-222; Y-224; C-258; Y-542; C-558;  
 RP C-578; C-728; C-985; C-1006; C-1031; C-1231 AND R-1261, AND VARIANTS  
 RP R-170; L-496; Q-1153; W-1183 AND A-2223.

RX MEDLINE=98049753; PubMed=9388399;  
 RA Joutel A., Vahedi K., Corpechot C., Tiesch A., Chabriat H.,  
 RA Vayssières C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,  
 RA Bach J.-F., Tournier-Lasserre E.;  
 RT "Strong clustering and stereotyped nature of Notch3 mutations in  
 RT CADASIL patients,"  
 RL Lancet 350:1511-1515(1997).

[5] VARIANT CADASIL 114-GUY--PRO-120 DEL.  
 RP MEDLINE=20264473; PubMed=10802807;  
 RX Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,  
 RA Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.,  
 RA "Splice site mutation causing a seven amino acid Notch3 in-frame  
 RT deletion in CADASIL";  
 RL Neurology 54:1874-1875 (2000).  
 RN [6]  
 RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Misiadis E., Henrique D., Carcangiu M.-L.,  
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.,  
 RT "Human ligands of the Notch receptor";  
 RL Am. J. Pathol. 154:785-794 (1999).  
 CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity).  
 CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -I- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult  
 CC tissues.  
 CC -I- PFM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -I- PFM: Phosphorylated (By similarity).  
 CC -I- DISEASE: Defects in NOTCH3 are associated with CADASIL (Cerebral  
 CC autosomal dominant arteriopathy with subcortical infarcts and  
 CC leukoencephalopathy) which causes a type of stroke and dementia of  
 CC which key features include recurrent subcortical ischemic events  
 CC and vascular dementia.  
 CC -I- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -I- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.  
 CC -I- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -I- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL; U97669; AB91371.1; --  
 DR EMBL; AF058900; AAC14346.1; --  
 DR EMBL; AF058881; AAC14346.1; JOINED.  
 DR EMBL; AF058882; AAC14346.1; JOINED.  
 DR EMBL; AF058883; AAC14346.1; JOINED.  
 DR EMBL; AF058884; AAC14346.1; JOINED.  
 DR EMBL; AF058885; AAC14346.1; JOINED.  
 DR EMBL; AF058886; AAC14346.1; JOINED.  
 DR EMBL; AF058887; AAC14346.1; JOINED.  
 DR EMBL; AF058888; AAC14346.1; JOINED.  
 DR EMBL; AF058889; AAC14346.1; JOINED.  
 DR EMBL; AF058890; AAC14346.1; JOINED.  
 DR EMBL; AF058891; AAC14346.1; JOINED.  
 DR EMBL; AF058892; AAC14346.1; JOINED.

DR EMBL; AF058893; AAC14346.1; JOINED.  
 DR EMBL; AF058894; AAC14346.1; JOINED.  
 DR EMBL; AF058895; AAC14346.1; JOINED.  
 DR EMBL; AF058896; AAC14346.1; JOINED.  
 DR EMBL; AF058897; AAC14346.1; JOINED.  
 DR EMBL; AF058898; AAC14346.1; JOINED.  
 DR EMBL; AF058899; AAC14346.1; JOINED.  
 DR EMBL; AC004257; AAC04897.1; --  
 DR EMBL; AC004663; AAC15789.1; --  
 DR HSSP; P00740; IEDM.  
 DR Genew; HGNC:7883; NOTCH3.  
 DR MIM; 600276; --  
 DR MIM; 125310; --  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF-II.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 3.  
 DR PRINTS; PR00010; EGFBL00D.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_CA; 19.  
 DR SMART; SM00001; EGF\_like; 14.  
 DR SMART; SM00004; NL\_3.  
 DR PROSITE; PS00088; ANK\_REPEAT; 4.  
 DR PROSITE; PS02097; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 18.  
 DR PROSITE; PS00022; EGF\_1; 33.  
 DR PROSITE; PS01186; EGF\_2; 25.  
 DR PROSITE; PS01187; EGF\_CA; 18.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;  
 KW Disease mutation.  
 FT SIGNAL 1 39  
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FT DOMAIN 924 960 EGF-LIKE 24.  
 FT DOMAIN 962 998 EGF-LIKE 25.  
 FT DOMAIN 1000 1034 EGF-LIKE 26.  
 FT DOMAIN 1047 1082 EGF-LIKE 27.

## Query Match

Best Local Similarity 34.5%; Score 174.5; DB 1; Length 2321;  
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY 56 CDGACGCTTATYRTAATYRSPGLAPAPRYAC-CRQKCR--TSGLPGACGAICQPPCR 112  
 DB 87 CAGGVCVCS-----SVVACTARFSCRCRGRFGPDCCSLPDPCC-----LSSPCA 129  
 QY 113 NGSSC-VOP-CR-CRCPACRGDTQCSVDDEC-----SARRGCGPQRCVNTAGSYWQCM 164  
 DB 130 HGARCSTVGPGRFLCSCPPGYGRSCRSVDCECRVGPCHGSG-----TCLNTGFSFRCCCP 186  
 QY 165 EGHSLADGTLVCPKRGPPRVANP 189  
 DB 187 AGYT-----GPLCENPAVP--CAPSP 205

## RESULT 14

NIDO HUMAN STANDARD; PRT; 1247 AA.

AC P14543; Q14942;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Nidogen precursor (Enactin).  
 GN NID.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

## SEQUENCE FROM N.A.

RA MEDLINE=90091745; Pubmed=2574658;  
 RA Nagayoshi T., Sanborn D., Hickok N.J., Olsen D.R., Fazio M.J.,  
 RA Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Uitto J.;  
 RT "Human nidogen: complete amino acid sequence and structural domains  
 RT deduced from cDNAs, and evidence for polymorphism of the gene.";  
 RL DNA 8:581-594 (1989).  
 RN [2]

## SEQUENCE FROM N.A.

RA MEDLINE=96044428; Pubmed=7557988;  
 RA Zimmermann K., Hoischen S., Hattner M., Nischt R.;  
 RT "Genomic sequences and structural organization of the human nidogen  
 RT gene (NID).";  
 RL Genomics 27:245-250 (1995).  
 RN [3]

## SEQUENCE OF 667-1247 FROM N.A.

RA TISSUE=Placenta;  
 RA MEDLINE=89270475; Pubmed=2471408;  
 RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,  
 RA Timpl R., Chu M.L., Uitto J.;  
 RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the  
 RT gene to chromosome 1q43.";  
 RL Am. J. Hum. Genet. 44:876-885 (1989).  
 RN [1]

CC -1- FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN  
 CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-  
 CC EXTRACELLULAR MATRIX INTERACTIONS.  
 CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 LDL-RECEPTOR WYTD DOMAINS.

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CC EMBL; M30269; AA559932.1; -  
 CC EMBL; X82245; CAAS7709.1; -  
 CC EMBL; X84819; CAAS7709.1; JOINED.  
 CC EMBL; X84820; CAAS7709.1; JOINED.  
 CC EMBL; X84821; CAAS7709.1; JOINED.  
 CC EMBL; X84822; CAAS7709.1; JOINED.  
 CC EMBL; X84823; CAAS7709.1; JOINED.  
 CC EMBL; X84824; CAAS7709.1; JOINED.  
 CC EMBL; X84825; CAAS7709.1; JOINED.  
 CC EMBL; X84826; CAAS7709.1; JOINED.  
 CC EMBL; X84827; CAAS7709.1; JOINED.  
 CC EMBL; X84828; CAAS7709.1; JOINED.  
 CC EMBL; X84829; CAAS7709.1; JOINED.  
 CC EMBL; X84830; CAAS7709.1; JOINED.  
 CC EMBL; X84831; CAAS7709.1; JOINED.  
 CC EMBL; X84832; CAAS7709.1; JOINED.  
 CC EMBL; X84833; CAAS7709.1; JOINED.  
 CC EMBL; X84834; CAAS7709.1; JOINED.  
 CC EMBL; X84835; CAAS7709.1; JOINED.  
 CC EMBL; X84836; CAAS7709.1; JOINED.  
 CC EMBL; X84837; CAAS7709.1; JOINED.  
 CC EMBL; M27445; AA577261.1; -  
 CC PIR; A33322; MMHUND.  
 CC HSSP; P35555; IEMN.  
 CC GENE; HGNC:7821; NID.  
 CC MIM; 131390; -  
 CC InterPro; IPR001552; Asx\_hydroxyl.  
 CC InterPro; IPR000561; EGF-like.  
 CC InterPro; IPR001881; EGF Ca.  
 CC InterPro; IPR000033; Ldl\_receptor\_rep.  
 CC InterPro; IPR003866; Nidogen\_ext.  
 CC Pfam; PF00008; EGF\_6.  
 CC Pfam; PF00058; Ldl\_recept\_b; 3.  
 CC Pfam; PF00066; thyroglobulin\_1; 1.  
 CC SMART; SM00179; EGF\_Ca; 2.  
 CC SMART; SM00001; EGF-like; 4.  
 CC SMART; SM00135; LY; 5.  
 CC SMART; SM00539; NIDO; 1.  
 CC SMART; SM00211; TY; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 CC PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
 CC PROSITE; PS00022; EGF\_1; 1.  
 CC PROSITE; PS01186; EGF\_2; 5.  
 CC PROSITE; PS01187; EGF\_Ca; 2.  
 CC K1 Basal membrane; Extracellular matrix; Glycoprotein; Sulfation;  
 CC K1 Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.  
 CC FT CHAIN 1 28  
 CC FT DOMAIN 29 1247  
 CC FT DOMAIN 670 917  
 CC FT DOMAIN 918 1247  
 CC FT DOMAIN 386 426  
 CC FT DOMAIN 668 709  
 CC FT DOMAIN 710 751  
 CC FT DOMAIN 758 801  
 CC FT DOMAIN 802 840  
 CC FT DOMAIN 872 919  
 CC FT DOMAIN 989 1030  
 CC FT DOMAIN 1032 1073  
 CC FT DOMAIN 1075 1118  
 CC FT DOMAIN 1124 1163  
 CC FT DOMAIN 1208 1244  
 CC FT MOD\_RES 289 289  
 CC FT MOD\_RES 296 296  
 CC FT DISULFID 672 685  
 CC FT DISULFID 679 695  
 CC FT DISULFID 697 708  
 CC FT DISULFID 714 727

CC NIDOGN.  
 CC I (LARGER GLOBULAR DOMAIN).  
 CC II (CYSTEINE-RICH).  
 CC III (SMALLER GLOBULAR DOMAIN).  
 CC EGF-LIKE 1.  
 CC EGF-LIKE 2.  
 CC EGF-LIKE 3.  
 CC EGF-LIKE 4.  
 CC EGF-LIKE 5.  
 CC THYROGLOBULIN TYPE I.  
 CC LDL-RECEPTOR WYTD MOTIF 1.  
 CC LDL-RECEPTOR WYTD MOTIF 2.  
 CC LDL-RECEPTOR WYTD MOTIF 3.  
 CC LDL-RECEPTOR WYTD MOTIF 4.  
 CC EGF-LIKE 6.  
 CC SULFATION (POTENTIAL).  
 CC SULFATION (POTENTIAL).  
 CC BY SIMILARITY.  
 CC BY SIMILARITY.  
 CC BY SIMILARITY.  
 CC BY SIMILARITY.

Tue Dec 17 14:03:52 2002

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FT DISULFID 721 736 BY SIMILARITY.
FT DISULFID 738 750 BY SIMILARITY.
FT DISULFID 762 777 BY SIMILARITY.
FT DISULFID 769 787 BY SIMILARITY.
FT DISULFID 789 800 BY SIMILARITY.
FT DISULFID 806 817 BY SIMILARITY.
FT DISULFID 826 839 BY SIMILARITY.
FT DISULFID 828 839 BY SIMILARITY.
FT DISULFID 1212 1233 BY SIMILARITY.
FT DISULFID 1219 1232 BY SIMILARITY.
FT DISULFID 1234 1243 BY SIMILARITY.
FT SITE 702 704 CELL ATTACHMENT SITE.
FT CARBOHYD 1137 1137 N-LINKED (GLCNAC.) (POTENTIAL).
FT CONFLICT 33 34 EL -> SS (IN REF. 2).
FT CONFLICT 37 42 FGPGQG -> SAPDR (IN REF. 2).
FT CONFLICT 1115 1115 H -> T (IN REF. 3).
FT CONFLICT 1115 1115 4681BSB3CEC1575B CRC64;
FT SEQUENCE 1247 AA; 136488 MW; 136488 MW; 4681BSB3CEC1575B CRC64;

Query Match 11.5%; Score 173.5; DB 1; Length 1247;
Best Local Similarity 25.8%; Pred. No. 6e-06; Indels 109; Gaps 18;
Matches 80; Conservative 23; Mismatches 98;

QY 20 TEHAYRGRV-----CAVRAHG-----DPVSESVQRYVQFLTCGHRACSTYR 66
Db 681 TNAACRPGPTQTFCESIGFRDGTCTVDIDECSE-----QF--SVCGSHTCNNH- 730
QY 67 TIVTAYRRSPGLAPRVPACPGWKRTSGLPGACGAACQPP-----CRNG----- 114
Db 731 -----PGTFRCCEVEGQFSD--EGTCVAVVDORPINYCETGLHNCIDIPQR 774
QY 115 GSCVQPG-----RCPCAGMRGD--TCQSDVDECSARCGCPORCVNTAGSYWCOCWGHGS 168
QY 775 AQCIYTGSSYTCSCLPFGSDGACQ--DVDECQPSRCHPDFAFCYNTPGSTFCQCKPGY- 832
Db 169 LSADGTLCLVP-----KGGPRVAPNPPTG----- 191
QY 833 -QGDFRCVPGVEKTEKCHEREHLGAAGATDPQPIPPGLFVPCDAGHYAFTOCHG 891
QY 192 -----VDSAMKEVQLQRVDLLBEKLQVLAPLH--SLASQALEHGLPDGSLVHS 243
Db 892 STGYCWCVDORGR-EVEGTRTPGWTPTCLSTVAPPIHOGPAVPTAVIPLP-PGTHLL-- 947
QY 244 FQGLGRIDSL 253
Db 948 FAQTGKIERL 957

RESULT 15
NTCI_MOUSE STANDARD; PRT; 2531 AA.
ID NTC1_MOUSE Q06007; Q06007; Q06007; Q06007; Q06007;
AC Q01705; Q09W58; Q09JUC2; Q06007; Q06007; Q06007; Q06007;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)
DE (mt14) (p300).
GN NOTCH1 OR NOTCH
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryo;
RX MEDLINE=93194170; PubMed=849489;
RA Franco del Amo F., Swiatek P.J., Jenkins N.A.,
RA Copeland N.G., Gridley T.;
RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse
RT homolog of Drosophila Notch."
RT Genomics 15:259-264 (1993).
RL [2]
RN SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
RP STRAIN=CD-1; TISSUE=Embryo;
RC

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RX MEDLINE=93050801; PubMed=1426644;
RA Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;
RA "Expression analysis of a Notch homologue in the mouse embryo.";
RL Dev. Biol. 154:377-387 (1992).
RN [3]
RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX MEDLINE=93048835; PubMed=1425352;
RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
RA Greenspan R.J., McMahon A.P., Gridley T.;
RA "Expression pattern of Notch, a mouse homolog of Drosophila Notch,
RT suggests an important role in early postimplantation mouse
RT development.";
RL Development 115:737-744 (1992).
RN [4]
RP SEQUENCE OF 1161-1547 FROM N.A.
RC STRAIN=CS7BL/6 X CBA; TISSUE=Embryo;
RX MEDLINE=93170563; PubMed=8440332;
RA Lardelli M., Lendahl U.; mouse Notch homologues coexpressed in a
RA "Notch A and Notch B-two mouse Notch homologues coexpressed in a
RT wide variety of tissues.";
RL Exp. Cell Res. 204:364-372 (1993).
RN [5]
RP SEQUENCE OF 1659-1673 FROM N.A.
RX MEDLINE=99364499; PubMed=10437788;
RA Lee J.S., Ishimoto A., Yanagawa S.I.;
RA "Murine leukemia provirus-mediated activation of the Notch1 gene leads
RT to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
RL FEBS Lett. 455:276-280 (1999).
RN [6]
RP SEQUENCE OF 1950-2201 FROM N.A.
RX MEDLINE=98029496; PubMed=9384671;
RA Messerle M., Folio M., Nehls M., Eggert H., Boehm T.;
RA "Dynamic changes in gene expression during in vitro differentiation of
RT mouse embryonic stem cells.";
RL Cytokines Cell. Mol. Ther. 1:139-143 (1995).
RN [7]
RP SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
RX MUTAGENESIS OF 1651-ARG-GLN-ARG-ARG-1654.
RX MEDLINE=98318619; PubMed=9653148;
RA Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
RA Israel A.;
RA "The Notch1 receptor is cleaved constitutively by a furin-like
RT convertase.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112 (1998).
RN [8]
RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21523956; PubMed=11518718;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
RA "Murine notch homologs (NL-4) undergo presenilin-dependent
RT proteolysis.";
RL J. Biol. Chem. 276:40268-40273 (2001).
RN [9]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=11459941;
RA Mizutani T., Taniuchi Y., Aoki T., Hashimoto N., Honjo T.;
RA "Conservation of the biochemical mechanisms of signal transduction
RT among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).
RN [10]
RP FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of differentiation, proliferation and
CC affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). May play an essential role in
CC postimplantation and/or differentiation. May be involved in mesoderm
CC specification and/or differentiation. Involved in the
CC development of both CD4+ and CD8+ cells in the thymus.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-
CC terminal fragment N(BC) which are probably linked by disulfide
CC bonds.

```

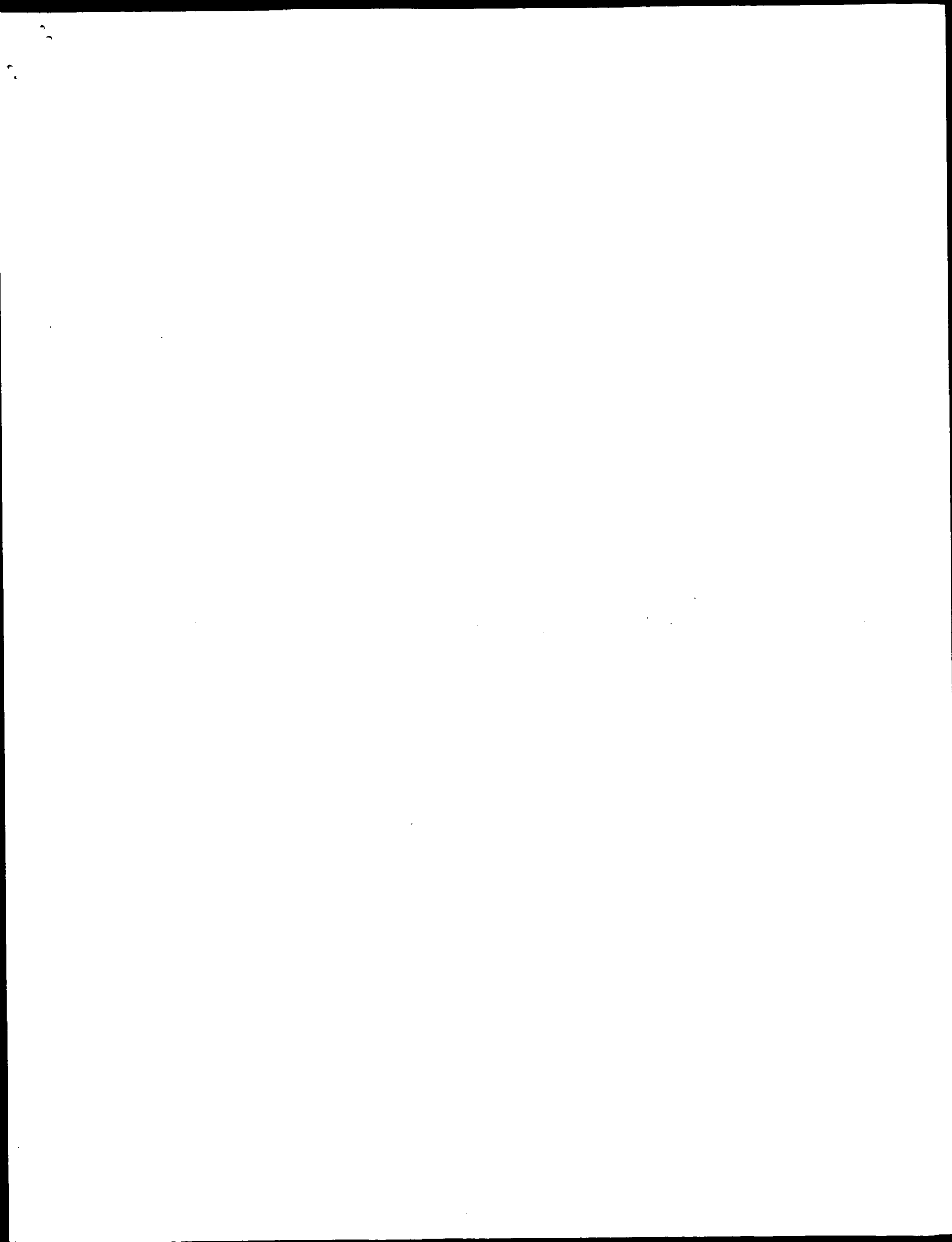


CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the brain, lung and  
 CC thymus. Expressed at lower levels in the spleen, bone-marrow,  
 CC spinal cord, eyes, mammary gland, liver, intestine, skeletal  
 CC muscle, kidney and heart.  
 CC -1- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 d.p.c.  
 CC By 8.5 d.p.c. highly expressed in presomitic mesoderm, mesenchyme  
 CC and endothelial cells, while much lower levels are seen in the  
 CC in the neuroepithelium. At 13.5 d.p.c. expressed at high levels  
 CC in the neuroepithelium. At 13.5 d.p.c. expressed in the surface  
 CC ectoderm, eye and developing whisker follicles.  
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(BC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane.  
 CC -1- PTM: Phosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use. By non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; Z11886; CAAT7941.1; -;  
 DR EMBL; L02613; AAK1498.1; -;  
 DR EMBL; X68278; CAA48339.1; -;  
 DR EMBL; AJ238029; CAA40733.1; -;  
 DR EMBL; X82562; CAA57909.1; -;  
 DR HSP; P00740; IDDM.  
 DR MGI; MGI:97363; Notch1.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Anx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 35.  
 DR Pfam; PF00023; ank; 7.  
 DR Pfam; PF00066; notch; 3.  
 DR PRINTS; PR00010; EGFBL00.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 3.  
 DR SMART; SM00179; EGF\_Ca; 23.  
 DR SMART; SM00001; EGF-like; 11.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 2.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 22.  
 DR PROSITE; PS00022; EGF\_1; 34.  
 DR PROSITE; PS01186; EGF\_2; 27.  
 DR PROSITE; PS01187; EGF\_Ca; 21.  
 DR Receptor; Transcription regulation; Activator; Differentiation;  
 KM Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KM Transmembrane; Glycoprotein; Signal; Phosphorylation;  
 KM Alternative splicing.  
 FT SIGNAL 1  
 FT 18 POTENTIAL.

|    |          |      |      |   |
|----|----------|------|------|---|
| FT | CHAIN    | 19   | 2531 | NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1. |
| FT | CHAIN    | 1711 | 2531 | NORCH EXTRACELLULAR TRUNCATION.           |
| FT | CHAIN    | 1744 | 2531 | NORCH INTRACELLULAR DOMAIN.               |
| FT | DOMAIN   | 15   | 1725 | EXTRACELLULAR (POTENTIAL).                |
| FT | TRANSHEM | 1726 | 1746 | POTENTIAL.                                |
| FT | DOMAIN   | 1747 | 2531 | CYTOPLASMIC (POTENTIAL).                  |
| FT | DOMAIN   | 20   | 58   | EGF-LIKE 1.                               |
| FT | DOMAIN   | 59   | 99   | EGF-LIKE 2.                               |
| FT | DOMAIN   | 102  | 139  | EGF-LIKE 3.                               |
| FT | DOMAIN   | 140  | 176  | EGF-LIKE 4.                               |
| FT | DOMAIN   | 178  | 216  | EGF-LIKE 5.                               |
| FT | DOMAIN   | 218  | 255  | EGF-LIKE 6.                               |
| FT | DOMAIN   | 257  | 293  | EGF-LIKE 7.                               |
| FT | DOMAIN   | 295  | 333  | EGF-LIKE 8.                               |
| FT | DOMAIN   | 335  | 371  | EGF-LIKE 9.                               |
| FT | DOMAIN   | 372  | 410  | EGF-LIKE 10.                              |
| FT | DOMAIN   | 412  | 450  | EGF-LIKE 11.                              |
| FT | DOMAIN   | 452  | 488  | EGF-LIKE 12.                              |
| FT | DOMAIN   | 490  | 526  | EGF-LIKE 13.                              |
| FT | DOMAIN   | 528  | 564  | EGF-LIKE 14.                              |
| FT | DOMAIN   | 566  | 601  | EGF-LIKE 15.                              |
| FT | DOMAIN   | 603  | 639  | EGF-LIKE 16.                              |
| FT | DOMAIN   | 641  | 676  | EGF-LIKE 17.                              |
| FT | DOMAIN   | 678  | 714  | EGF-LIKE 18.                              |
| FT | DOMAIN   | 716  | 751  | EGF-LIKE 19.                              |
| FT | DOMAIN   | 753  | 789  | EGF-LIKE 20.                              |
| FT | DOMAIN   | 791  | 827  | EGF-LIKE 21.                              |
| FT | DOMAIN   | 829  | 867  | EGF-LIKE 22.                              |
| FT | DOMAIN   | 869  | 905  | EGF-LIKE 23.                              |
| FT | DOMAIN   | 907  | 943  | EGF-LIKE 24.                              |

Query Match 11.4%; Score 172; DB 1; Length 2531;  
 Best Local Similarity 34.5%; Pred. No. 1.6e-05;  
 Matches 41; Conservative 5; Mismatches 37; Indels 36; Gaps 5;  
 DB 129 CSPGMSGKS-----CQADPCASNPANGGGCLFFESSYICRCRPGHGPCRDP 178  
 QY 88 CCGMKRTSGLPACGAALICP-----PCRRGSCV---OPGRCPAGMRGDTQSD 137  
 QY 138 VDECSARRGCGCP--RCVUTAGSYNQCMWEGH-----SIADGTLVCPVK 180  
 DB 179 VNECSNPGLCRHGHCHNEISYRCACCATHTGPHCELPVPCSPSPSCNGATCRPTG 217

Search completed: December 17, 2002, 10:01:58  
 Job time : 10.8065 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on:

December 17, 2002, 09:58:37 ; Search time 28.4915 Seconds  
(without alignments)  
1974.306 Million cell updates/sec

Title:  
US-09-852-472-2

Sequence: 1 MRGQEVLMMLVAVGCT.....SEQISFLERQLGSCSKKDS 273

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

SPRMBL 21  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_protist:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriophage:  
17: sp\_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID     | Description        |
|------------|--------|-------------|--------|-----------|--------------------|
| 1          | 1505   | 100.0       | 273    | 4 Q9UHF1  | Q9UHF1 homo sapien |
| 2          | 1504   | 99.9        | 273    | 4 Q9GEG0  | Q9GEG0 homo sapien |
| 3          | 1181   | 78.5        | 278    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 4          | 1104.5 | 73.4        | 265    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 5          | 728.5  | 48.4        | 190    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 6          | 434.5  | 28.9        | 293    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 7          | 422.5  | 28.1        | 293    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 8          | 276.5  | 18.4        | 509    | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 9          | 276.5  | 18.4        | 512    | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 10         | 257    | 17.1        | 1574   | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 11         | 253.5  | 16.8        | 558    | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 12         | 252.5  | 16.8        | 553    | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 13         | 246.5  | 16.8        | 554    | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 14         | 246.5  | 16.8        | 550    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 15         | 223    | 14.8        | 561    | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 16         | 219    | 14.6        | 1664   | 5 Q9GCT5  | Q9GCT5 mus musculu |

|    |       |      |      |           |                    |
|----|-------|------|------|-----------|--------------------|
| 17 | 218.5 | 14.5 | 578  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 18 | 217.5 | 14.5 | 528  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 19 | 197.5 | 13.1 | 592  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 20 | 197   | 13.1 | 747  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 21 | 197   | 13.1 | 1034 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 22 | 195   | 13.0 | 1034 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 23 | 193   | 12.8 | 609  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 24 | 189   | 12.6 | 678  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 25 | 184   | 12.2 | 673  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 26 | 184   | 12.2 | 674  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 27 | 183.5 | 12.2 | 2906 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 28 | 182.5 | 12.1 | 648  | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 29 | 182.5 | 12.1 | 701  | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 30 | 182.5 | 12.1 | 816  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 31 | 182   | 12.1 | 1764 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 32 | 182   | 12.1 | 2809 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 33 | 181.5 | 12.1 | 815  | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 34 | 179   | 11.9 | 418  | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 35 | 178.5 | 11.9 | 4555 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 36 | 178   | 11.8 | 674  | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 37 | 177.5 | 11.8 | 3138 | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 38 | 177   | 11.8 | 4215 | 5 Q9GCT5  | Q9GCT5 mus musculu |
| 39 | 176   | 11.7 | 1511 | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 40 | 175   | 11.6 | 1587 | 4 Q9GCT5  | Q9GCT5 mus musculu |
| 41 | 174.5 | 11.6 | 1095 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 42 | 174.5 | 11.6 | 3857 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 43 | 173.5 | 11.5 | 1833 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 44 | 173.5 | 11.5 | 2872 | 11 Q9GCT5 | Q9GCT5 mus musculu |
| 45 | 172   | 11.4 | 1212 | 13 Q9GCT5 | Q9GCT5 mus musculu |

## ALIGNMENTS

## RESULT 1

Q9UHF1 PRELIMINARY; PRT; 273 AA.

Q9UHF1  
AC Q9UHF1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE NOTCH4-like protein (Hypothetical 29.6 kDa protein).  
GN ZNF101 OR DKFP58612317.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
NC NCBI TaxID=9606;  
LN 1  
RP SEQUENCE FROM N.A.  
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehnert J.,  
RA Chhabra P.  
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RC TISSUE=UTERUS.  
RA Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL EMBL; AF186111; AA01429.1; -;  
DR EMBL; AL512735; CAC21666.1; -;  
DR HSSP; P08709; IFAK.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PF00081; EGF\_Ca.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
SQ SEQUENCE 273 AA; 29617 MW; 5740BB845ED5A988 CRC64;

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Query Match 100.0%; Score 1505; DB 4; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.2e-130; Indels 0; Gaps 0;  
Matches 273; Conservative 0; Mismatches 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 60  
DB 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 60

QY 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
DB 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 120

QY 121 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180  
DB 121 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273  
DB 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273

RESULT 2  
ID Q96EG0 PRELIMINARY; PRT; 273 AA.  
AC Q96EG0;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Similar to NEU1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RN STRAUSBERG R.;  
RC TISSUE=OVARY;  
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC012377; AAH12377.1; --  
DR InterPro; IPR000152; ASX hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR Pfam; PF00008; EGF; 2.  
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
SQ SEQUENCE 273 AA; 5AD0A4845ED5B688 CRC64;

Query Match 99.9%; Score 1504; DB 4; Length 273;  
Best Local Similarity 99.6%; Pred. No. 1.4e-130; Indels 0; Gaps 0;  
Matches 272; Conservative 1; Mismatches 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 60  
DB 1 MRGSEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 60

QY 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
DB 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 120

QY 121 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180  
DB 121 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273  
DB 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273

RESULT 3  
ID Q9QXT5 PRELIMINARY; PRT; 278 AA.  
AC Q9QXT5;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE NOTCH4-like protein (Vascular endothelial zinc finger 1).  
GN VEZF1 OR ZNEU1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
RN SHEPPARD P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
RA O'Hara P.;  
RT "Mus musculus homolog of HLA class III region containing NOTCH4  
gene.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
RN Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
RA Martinez T., Hoffman R., O'Hara P.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
RN STRAUSBERG R.;  
RC TISSUE=LIVER;  
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF184973; AA01322.1; --  
DR EMBL; BC024610; AAH24610.1; --  
DR HSP; P00740; 1EDW.  
DR MGD; MGI:1313291; Vezf1.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR Pfam; PF00008; EGF; 2.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00001; EGF-like; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.  
SQ SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

Query Match 78.5%; Score 1181; DB 11; Length 278;  
Best Local Similarity 78.1%; Pred. No. 8.2e-101;  
Matches 214; Conservative 18; Mismatches 40; Indels 2; Gaps 2;

QY 1 MRGSEVLLMVLAVGG-TEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 59  
DB 4 MRGSEVLLMVLAVGG-TEHAYRPGRRVCAVRAHGDVPVSEFVQRYQPFLLTCDGHR 63

QY 60 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 119  
DB 64 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQP 123

QY 120 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 179  
DB 124 GRCPAGWGDTCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 183

QY 180 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 238  
DB 184 GPPRVAPNPTGVDSAMKEEVQRLQSVLDLLEKQLVLAPLHSLASQALEHGLPDPGSL 243

QY 239 LLVHSFQOLGRIDSLSQISFLEEQSGSCCKD 272  
DB 244 LLVHSFQOLGRIDSLSQISFLEEQSGSCCKD 277

RESULT 4  
ID 09DCPS PRELIMINARY; PRT; 265 AA.  
AC 09DCPS.  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
CN Vascular endothelial zinc finger 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RA MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Aizawa K., Iizawa M., Nishii K., Kiyosawa H., Kondo S., Yamana K.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Sakai K., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
Blake J., Boileau D., Boujard M., Kono H., Baldarelli R., Barish G.,  
Bradenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,  
Guenther S., Hill D., Hofmann M., Hume D.A., Kimura M., Lee N.H.,  
Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,  
Norio P., Ring B., Ringwald C., Rodriguez C., Sessa T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weiler C., Whitaker C., Wilming L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,  
Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL: AK002601; BAB2222.1;  
DR HSSP: P00740; 1EDM.  
DR MGI: 1313291; Vezfi.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001881; EGF\_Ca.  
DR Pfam: PF00008; EGF\_2.  
DR SMART: SM00181; EGF\_2.  
DR SMART: SM00002; EGF\_1like; 2.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE: PS01187; EGF\_Ca; 1.  
SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA848F97E CRC64;

Query Match  
Best Local Similarity 73.4%; Score 1104.5; DB 11; Length 265;  
Matches 203; Conservative 17; Mismatches 39; Indels 15; Gaps 3;  
QY 1 MRCSEVLLMVLAVG-TEHAYRGRVCAVRAGDPVSESTVQRYVOPFLTTCDG 59  
DB 4 MMSGELVAMFLVADGTEHYRPSRVCYIGSGISSEFFVQRYVOPFLTTCDG 59  
QY 60 RACSTYRTITVTRRSBGLAPRPVACCPGKRTSGLPACCAACOPPCNGSCVQ 119  
DB 64 RACSTYRTITVTRRSBGLAPRPVACCPGKRTSGLPACCAACOPPCNGSCVQ 119  
QY 120 PGRGCPAGRGDTCSQDVDECSARAGGCPORCVNTAGSYWCQMGSHSLADGTLVCPK 179  
DB 124 PGRGCPAGRGDTCSQDVDECSARAGGCPORCVNTAGSYWCQMGSHSLADGTLVCPK 179  
QY 180 GGPRAVNPNT-GVSGAMKEVQRIQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGS 238  
DB 184 EGSPVAPNPNTGVSGAMKEVQRIQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGS 238  
QY 239 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272  
DB 239 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272

Db 244 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 264

RESULT 5  
ID 09JWK3 PRELIMINARY; PRT; 190 AA.  
AC 09JWK3.  
DT 01-OCT-2000 (TEMBLrel. 15, Created)  
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
CN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.,  
"Cloning and Characterization of a Novel 20.4kd Estrogen-regulated  
protein in the Rat Spleen."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Marcantonio D., Huynh H.T.,  
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF23678; AAF5352.1;  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; Asx\_hydroxyl.  
DR InterPro: IPR001881; EGF-like.  
DR Pfam: PF00008; EGF\_2.  
DR SMART: SM00179; EGF\_Ca; 1.  
DR SMART: SM00010; ASX\_HYDROXYL; 1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE: PS01187; EGF\_Ca; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1B998 CRC64;

Query Match  
Best Local Similarity 48.4%; Score 728.5; DB 11; Length 190;  
Matches 131; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
QY 105 AICPPCRVGGSCVQPPGRCPCPAGMRGDTCSQDVDECSARAGGCPORCVNTAGSYWCQW 164  
DB 21 AICPPCRVGGSCVQPPGRCPCPAGMRGDTCSQDVDECSARAGGCPORCVNTAGSYWCQW 164  
QY 165 EGHSLADGTLVCPKGGPPVAPNPNT-GVDSAMKEVQRIQSRVLDLEKQLVLAFLHSLASQ 223  
DB 81 EGHSLADGTLVCPKGGPPVAPNPNT-GVDSAMKEVQRIQSRVLDLEKQLVLAFLHSLASQ 223  
QY 224 LASQALHGLPDPGSHLVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272  
DB 141 LASQALHGLPDPGSHLVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272  
RESULT 6  
ID 035447 PRELIMINARY; PRT; 293 AA.  
AC 035447.  
DT 01-JAN-1998 (TEMBLrel. 05, Created)  
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
DE Hypothetical 32.1 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]

us-09-852-472-2.ispt

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SEQUENCE FROM N.A.  
 RP Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.,  
 RA "Sequence of the mouse major histocompatibility locus class III  
 RT region." (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF030001; A882010.1; --  
 DR HSP: P35555; IEMN.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR00008; EGF; 2.  
 DR Pfam: PF00008; EGF; 2.  
 DR SMART: SM00179; EGF\_Ca; 1.  
 DR SMART: SM00001; EGF-like; 1.  
 DR PROSITE: PS00010; ASX HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_Ca; 1.  
 DR PROSITE: PS01187; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 KW Hypothetical protein; Repeat.  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 293 AA; 32066 MW; 8A99A5EC000A2C62 CRC64;  
 Query Match 28.9%; Score 434.5; DB 11; Length 293;  
 Best Local Similarity 37.3%; Pred. No. 5e-32; Mismatches 101; Indels 51; Gaps 14;  
 Matches 112; Conservative  
 Y 1 MRGQEVLLWLLVLAAG-GTE-HAYRGRVCAVRAHGDV--SESFQVRYQFLTTC 56  
 D 11 LRG-----LSFFLLVMTGEGTGGSGKSLGVCSTQLLVPLRYNESYQPVYKFLTLC 65  
 Y 57 DGRACSTYRTYTVARVSPGLAPRYACCPGKWTSLPGACGA-AICOPPCRRGG 115  
 D 66 AGRRICSTYRTYTVARVREVRV-P-QTHVCCQGWKKPH--PGALTCDAICSKPCING 122  
 Y 116 SCVQRCRCAPAGRGDTCQSDVDCSARRGCPQRCVNTAGSYWCQWEGHSLSDGTL 175  
 D 123 VCTGPRCPCAPGCGKHKHVDVDCRASLTLCSHGLNTLGLSCFPHLVGLDGT 182  
 Y 176 CVFPGGPPRVANPTGV-----DSAMKEEVQRLQSRVDLLEKQLVLAPL 221  
 D 183 CA--GGPE--SPTSASLTVAVREADSEERALKRVAELGRLEKLEQ----- 228  
 Y 222 HSLASQA--LEHGLP-DPGSLLVHVSFOQL-----GRDLSLSEQISFLBQLGSCSKKDS 273  
 D 229 --WATQAGWVRAVLPMPPELRPEQVAELWGRDRIESLSDQVLLLEERLGACEDNS 286  
 Query Match 28.1%; Score 422.5; DB 4; Length 293;  
 Best Local Similarity 36.5%; Pred. No. 6.3e-31; Mismatches 107; Indels 35; Gaps 10;  
 Matches 103; Conservative  
 Y 12 LLVAVGTEHAYRGRVCAVRAHGDV--SESFQVRYQFLTTCGHRACSTYRTY 69  
 D 19 LLIPGEGAKGSLRESQGVCSKQTLVPLRYNESYQPVYKFLTLCAGRRICSTYRTY 78  
 Y 70 RTAYRSPGLAPRYACCPGKWTSLPGCA--CGAICOPPCRRGGSCVQRCRCRCPA 127  
 D 79 RVMM-REVREVOQTHAVCCQGWKKRH--PGALTC-EAICAKPCLNGGVCAVRDQCEAP 134  
 Y 128 GWRGDTQSDVDCSARRGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKGSPRPVAP 187  
 D 135 GWGKHKCHVDVDCRTSITLCSHHCNTAGSFTCCPHDLVLVGLDGTCEGSPPEPTSA 194  
 Y 188 NPTGV-----DSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQA--LEHGLP-D 235  
 D 195 SILSVAVREAEKDERALKQRIHELGRLEKLEQ-----WAGQAGWVRAVLPVP 243  
 Y 236 PGSLLVHVSFOQL-----GRDLSLSEQISFLBQLGSCSKKDS 273  
 D 244 PEELQPEQVAELWGRDRIESLSDQVLLLEERLGACEDNS 285  
 RESULT 8  
 Q9VZD0 PRELIMINARY; PRT; 509 AA.  
 ID Q9VZD0 (TrEMBLrel. 13, Created)  
 AC Q9VZD0; 2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CG7447 protein.  
 GN Drosophila melanogaster (Fruit fly).  
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Eukaryota; Metazoa; Arthropoda; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-BERKELEY;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RX Adams M.D., G. Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Amanatides P.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA George R.A., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X., Pfeiffer B.D.,  
 RA Sutton G.G., Rogers Y.-H.C., Blazek R.G., Nelson C.R., Miklos G.L.G.,  
 RA Brandon R.C., Baxter E.G., Heit G., Andrews-Pfannkuch C., Baldwin D.,  
 RA Wan K.H., Doyle C., Agbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,  
 RA Arif J.F., Baxendale J., Bhandari D., Brodstein P., Brottier P.,  
 RA Balow R.M., Basu A.V., Berman B.P., Brodstein P., Brottier P.,  
 RA Beeson K.Y., Bosan P.V., Bouck J., Cadieu E., Center A., Chandra I.,  
 RA Borkova D., Botchan M.R., Butler H., Cadenot L.B., Davies P.,  
 RA Butts J.M., Cawley S., Dalka Z., Davenport L.B., Dew I., Dietz S.M.,  
 RA Butts J.M., Cawley S., Dalka Z., Davenport L.B., Dew I., Dietz S.M.,  
 RA De Fabos B., Delcher A., Deng Z., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Farkas N.S., Gelbart W.M., Glaser K.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Guan P., Harris M.,  
 RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston F., Karpman G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Hostin D., Houston F., Karpman G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mouton S.M., Moshina N.V., Mobarry C., Morris J., Moshir A.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Patel J.M.,  
RA Palazzolo M., Peltman G.S., Pan S., Pollard J.R., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheider F., Shen H.,  
RA Sier E., Spindler A.C., Stimpson M., Skupski M.P., Smith T.,  
RA Svirskas R., Tector A.C., Stapleton M., Strong R., Sun E.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu X., Yang S., Yao Q.A.,  
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Zhao S.,  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
DR EMBL: A6003481; AAF47894.1; -  
DR HSPB; P00740; IEDM.  
DR FlyBase; FBgn0035539; CG7447.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PFO0008; EGF\_2.  
DR SMART; SM00179; EGF\_CA.1.  
DR PROSITE; PS00001; ASX\_HYDROXYL.1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA.1.  
KW Calcium-binding; EGF-like domain.  
SQ SEQUENCE 509 AA; 57413 MW; E4782E4A6E121F0 CRC64;  
  
Query Match 18.4%; Score 276.5; DB 5; Length 509;  
Best Local Similarity 27.4%; Pred. No. 3.3e-17;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
  
Qy 28 RRYC-AVRAGDPV--SESFVQRYOPFLTTCD---GHRACSTYRTITYTAYRSPGLA 80  
Db RHICMOQRTVTMPVATRTVSRPTMKHVAATPCPTFGSCQCTRVQVHQAAYRVIDHK 301  
Qy 81 PAPP-RVACPCGMRKRTGGLPGACGAATCQPCRNAGSCVQPCRCPCAGMRDPTQSDVD 139  
Db 302 TAQOMTYDCTCGMSRBNPBSDCKMPCISARCONGAGCTAPSTCSPFTGRFCEDVD 364  
Qy 140 ECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPKGPBPVAVN-----P 189  
Db 362 ECQTER-PCDQCCINTHSGYFCRCRQGFVLSDQSC-----KVSTNADDAFEARDE 414  
Qy 190 TGVDSAMKEEVRQLOS-----RVDLSEKIQVLAPLHSLASQ--ALBGLPDRG 237  
Db 415 NDIDDTDAVATRLQKTEKSLANERVHTLQKSLQATYSVVDLTKSRISTLEKQADVS 474  
Qy 238 SLVHSPFOQLGRISLSEQISFL 260  
Db 475 RLQTLNLYKTESRTNKLGMNL 497

RC STRAIN-BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Patel J., Paragas V., Park S., Phuenavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY061220; AAL28768.1; -  
DR FlyBase; FBgn0035539; CG7447.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PFO0008; EGF\_2.  
DR PROSITE; PS00010; ASX\_HYDROXYL.1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 2.  
DR PROSITE; PS01187; EGF\_CA; UNKNOWN 1.  
SQ SEQUENCE 512 AA; 57770 MW; 4DD372EA6FE7627 CRC64;  
  
Query Match 18.4%; Score 276.5; DB 5; Length 512;  
Best Local Similarity 27.4%; Pred. No. 3.4e-17;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
  
Qy 28 RRYC-AVRAGDPV--SESFVQRYOPFLTTCD---GHRACSTYRTITYTAYRSPGLA 80  
Db RHICMOQRTVTMPVATRTVSRPTMKHVAATPCPTFGSCQCTRVQVHQAAYRVIDHK 304  
Qy 81 PAPP-RVACPCGMRKRTGGLPGACGAATCQPCRNAGSCVQPCRCPCAGMRDPTQSDVD 139  
Db 302 TAQOMTYDCTCGMSRBNPBSDCKMPCISARCONGAGCTAPSTCSPFTGRFCEDVD 364  
Qy 140 ECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPKGPBPVAVN-----P 189  
Db 362 ECQTER-PCDQCCINTHSGYFCRCRQGFVLSDQSC-----KVSTNADDAFEARDE 414  
Qy 190 TGVDSAMKEEVRQLOS-----RVDLSEKIQVLAPLHSLASQ--ALBGLPDRG 237  
Db 415 NDIDDTDAVATRLQKTEKSLANERVHTLQKSLQATYSVVDLTKSRISTLEKQADVS 474  
Qy 238 SLVHSPFOQLGRISLSEQISFL 260  
Db 478 RLQTLNLYKTESRTNKLGMNL 500

RESULT 10  
ID 088281 PRELIMINARY; PRT; 1574 AA.  
AC 088281  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DE MEGFE.  
GN MEGFE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DANLEY; TISSUE=BRAIN;  
RA MEDLINE=98360089; PubMed=9693030;  
RA Nakayama M., Nakajima D., Nagase T.,  
RT "Identification of high-molecular-weight proteins with multiple EGF-  
RL like motifs by motif-trap screening,"  
DR EMBL: AB011532; BA332462.1; -  
DR HSPB; P00736; IAPQ.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PFO0008; EGF\_2.  
DR SMART; SM00179; EGF\_CA.1.  
DR SMART; SM00001; EGF-like; 19.

1



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DE Hypothetical 61.4 kDa protein.
GN W80.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TERATOCARCINOMA/NEURON;
RA Franco B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TERATOCARCINOMA/NEURON;
RA MEDLINE=20241927; PubMed=10777661;
RT Buchner G., Orfanelli U., Quadrelli N., Bassi M.T., Andolfi G.;
RT "Identification of a new EGF-repeat-containing gene from human Xp22:
RT Genomics 65:16-23(2000).";
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AJ245671; CAB92132.1; -.
DR HSSP; P00736; IAPQ.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_Like; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
SQ SEQUENCE 554 AA; 6138 MW; D519238F2A604101 CRC64;

Query Match
Best Local Similarity 16.8%; Score 252.5; DB 4; Length 554;
Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;

QY 58 GHACRCYRTTYTAVRSPGLAPARPRYACCPGKRTSGLPACGALIQPCRNNGSGC 117
DB 21 GNASAHHGLASA--RQPGVCHYGTGLACCTGRRNS--KGVG-EATCEPCK-FGEC 74
QY 118 VOPGRCPAGWRGDTCCQSDVDECSARRGCGPQRCVNTAGSYWCOCWEGHSLADGTL 177
DB 75 VGPNCRCRCPGYTGKTCSDVDNECGMKRPPQHRCVNTHGSYKFCLSGHMLMPDPT-CV 133
QY 178 -----PRGQPP-----RVAPN 188
DB 134 NSRTAMINCOYSCDETEGPGCLCPSSGLRLAPN 168

RESULT 14
OS 09J325 PRELIMINARY; PRT; 550 AA.
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 61.5 kDa protein.
GN EGFL6 OR W80.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Franco B.;

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RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20241927; PubMed=10777661;
RA Buchner G., Orfanelli U., Quadrelli N., Bassi M.T., Andolfi G.;
RT "Identification of a new EGF-repeat-containing gene from human Xp22:
RT Genomics 65:16-23(2000).";
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AJ245672; CAB92138.1; -.
DR HSSP; P35555; IEMN.
DR MGD; MGJ1858599; EGFL6.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_Like; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
SQ SEQUENCE 550 AA; 61520 MW; DEF936325C9F31B3 CRC64;

Query Match
Best Local Similarity 16.4%; Score 246.5; DB 11; Length 550;
Matches 52; Conservative 12; Mismatches 50; Indels 27; Gaps 4;

QY 71 TAVRSPGLAPARPRYACCPGKRTSGLPACGALIQPCRNNGSCVOPGRCPAGWR 130
DB 30 SALAHQPGVCGYGTGMACCKYKRN--KGVG-EAMCEPRCK-FGECVGPNCRCRCPGYT 85
QY 131 GDTCCSDVDECSARRGCGPQRCVNTAGSYWCOCWEGHSLADGTL----- 175
DB 86 GKTCTVDVNECGVKKRPPQHRCVNTHGSYKFCLSGHMLPDPATNSRTARLNQYCC 145
QY 176 -----CVPRGQPPRVAPN 188
DB 146 EDTREGPRCPVSSGLRLGN 166

RESULT 15
OS 091V88 PRELIMINARY; PRT; 561 AA.
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE POEM (NEPHRORECTIN short isoform).
GN NPVT OR POEM OR NEPHL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Morimura N., Tezuka Y., Watanabe N., Yasuda M., Miyazaki S.;
RT "Molecular cloning of POEM, A novel adhesion molecule that interacts
RT with alpha8beta1 integrin.";
RL J. Biol. Chem. 276:42172-42181(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH SWISS; TISSUE=KIDNEY;
RX MEDLINE=21363579; PubMed=11470831;

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us-09-852-472-2.rspt

Tue Dec 17 14:03:52 2002

RA Brandenberger R., Schmidt A., Linton J., Wang D., Backus C., Denda S.,  
 RA Muller U., Reichardt L.F.,  
 RT "Identification and characterization of a novel extracellular matrix  
 RT protein nephronectin that is associated with integrin alpha8beta1 in  
 RT the embryonic kidney.",  
 RL J. Cell Biol. 154:447-458 (2001).  
 CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL; AB059656; BAB69692.1; -.  
 DR EMBL; AY035898; AAK96010.1; -.  
 DR MGD; MGI:2148811; Npnt.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR000998; MAM\_domain.  
 DR InterPro; IPR00008; EGF; 4.  
 DR Pfam; PF00629; MAM; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_3.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_3.  
 DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_3.  
 DR PROSITE; PS00060; MAM\_2; 1.  
 DR GlycoPDB.  
 KW Glycoprotein.  
 SQ SEQUENCE 561 AA; 61490 MW; 69E7ACAA0EE3F506 CRC64;  
 Query Match 14.8%; Score 223; DB 11; Length 561;  
 Best Local Similarity 43.4%; Pred. No. 3.2e-12;  
 Matches 43; Conservative 12; Mismatches 40; Indels 4; Gaps 3;  
 QY 76 SPGLAPARPRVACCPGWKRTSGLPAGCAAIQPPCNGGSCVQPCRCPCPAGWRGDTCC 135  
 DB 32 SIGLCRYGGRIDCCGWARGSW--GQC-QVVCQPCKH-GEVGNKCKCHPGFAGKTCN 87  
 QY 136 SDVDECSARRGCGPQRCVNTAGSYWCOCWEGHSLSDGT 174  
 DB 88 QDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGS 126

Search completed: December 17, 2002, 10:03:01  
 Job time : 32.4915 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 09:44:11 ; Search time 30.3643 Seconds

(without alignments)  
114.652 Million cell updates/sec

Title: US-09-852-472-3

Perfect score: 1411  
Sequence: 1 TEHAYPERVCAVRAHGD... SEQISFLEQLGSCCKSDS 254

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Fastest list 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 1411  | 100.0       | 254    | 20    | AAW8382     |
| 2          | 1411  | 100.0       | 273    | 20    | AAV41771    |
| 3          | 1411  | 100.0       | 273    | 20    | AAW8381     |
| 4          | 1411  | 100.0       | 273    | 21    | AAW4327     |
| 5          | 1411  | 100.0       | 273    | 21    | AAW18675    |
| 6          | 1411  | 100.0       | 273    | 21    | AAW24044    |
| 7          | 1411  | 100.0       | 273    | 21    | AAW01376    |
| 8          | 1411  | 100.0       | 273    | 22    | AAW2391     |
| 9          | 1411  | 100.0       | 273    | 22    | AAW61609    |
| 10         | 1410  | 99.9        | 273    | 20    | AAV41769    |

|    |        |      |     |    |          |                     |
|----|--------|------|-----|----|----------|---------------------|
| 11 | 1410   | 99.9 | 273 | 20 | AAV41770 | Human PRO1330 prot  |
| 12 | 1410   | 99.9 | 273 | 21 | AAW4325  | Human PRO213-1 pro  |
| 13 | 1410   | 99.9 | 273 | 21 | AAW4326  | Human PRO1330 prot  |
| 14 | 1410   | 99.9 | 273 | 21 | AAW18673 | Amino acid sequenc  |
| 15 | 1410   | 99.9 | 273 | 21 | AAW18674 | Amino acid sequenc  |
| 16 | 1410   | 99.9 | 273 | 21 | AAW24042 | Human PRO1330 prote |
| 17 | 1410   | 99.9 | 273 | 21 | AAW24043 | Human PRO1330 prote |
| 18 | 1410   | 99.9 | 273 | 21 | AAW52137 | Human TANGO 125 (T  |
| 19 | 1410   | 99.9 | 273 | 23 | AAW21079 | Human T125 (TANGO-  |
| 20 | 1410   | 99.9 | 273 | 23 | AAW83680 | Human PRO protein,  |
| 21 | 1392   | 98.7 | 251 | 23 | AAW21080 | Human T125 (TANGO-  |
| 22 | 1333   | 94.5 | 295 | 23 | AAW41685 | Human PRO1330 prote |
| 23 | 1333   | 94.5 | 295 | 21 | AAW41685 | Human PRO1330 prote |
| 24 | 1333   | 94.5 | 295 | 23 | AAW83609 | Human PRO1330 prote |
| 25 | 1333   | 94.5 | 295 | 23 | AAW83609 | Human PRO1330 prote |
| 26 | 1333   | 94.5 | 295 | 23 | AAW83609 | Human PRO1330 prote |
| 27 | 1187   | 87.7 | 224 | 20 | AAW59870 | Human normal uteru  |
| 28 | 1158.5 | 82.1 | 234 | 21 | AAW41644 | Human ORFX ORF1408  |
| 29 | 1139.5 | 80.8 | 255 | 20 | AAW8397  | Human secreted pro  |
| 30 | 1139.5 | 80.8 | 275 | 21 | AAW52141 | Mouse neuro-growth  |
| 31 | 1138.5 | 80.8 | 275 | 23 | AAW21081 | Mouse TANGO 125 (T  |
| 32 | 1138.5 | 80.8 | 275 | 23 | AAW21081 | Mouse T125 (TANGO-  |
| 33 | 1139.5 | 80.8 | 278 | 20 | AAW8392  | Mouse neuro-growth  |
| 34 | 1032.5 | 73.2 | 255 | 23 | AAW72368 | Mouse Notch4-like   |
| 35 | 1006   | 71.3 | 265 | 21 | AAW42204 | Murine protein iso  |
| 36 | 945.5  | 67.0 | 287 | 22 | AAW16977 | Human ORFX ORF1968  |
| 37 | 945.5  | 67.0 | 288 | 22 | AAW10533 | Human novel secret  |
| 38 | 945.5  | 67.0 | 288 | 22 | AAW18135 | Human CDNA SEQ ID   |
| 39 | 945.5  | 67.0 | 288 | 22 | AAW17049 | Human novel secret  |
| 40 | 945.5  | 67.0 | 288 | 22 | AAW19910 | Human novel secret  |
| 41 | 945.5  | 67.0 | 314 | 22 | AAW10362 | Human novel secret  |
| 42 | 931    | 66.0 | 169 | 20 | AAW8390  | Human CDNA SEQ ID   |
| 43 | 924    | 65.5 | 158 | 20 | AAW8388  | Human Znu1 partia   |
| 44 | 920.5  | 65.2 | 151 | 20 | AAW8391  | Human Znu1 partia   |
| 45 | 919.5  | 65.2 | 247 | 21 | AAW52139 | Human TANGO 125b (  |

#### ALIGNMENTS

|          |  |  |
|----------|--|--|
| RESULT 1 | AAW8382  | standard; Protein; 254 AA.                           |
| ID       | AAW8382  |  |
| AC       | AAW8382  |  |
| XX       |  |  |
| DT       | 26-Apr-1999  | (first entry)  |
| XX       |  |  |
| DE       | Human neuro-growth factor-like protein Zneu1 mature polypeptide.   |  |
| XX       |  |  |
| KW       | Zneu-1; neuro-growth factor-like protein; human; breast cancer; glioblastoma; pituitary adenoma; Alzheimer's disease; therapy; nerve regeneration; haematopoiesis; fertility; contraception; |  |
| KW       | antibody.  |  |
| XX       |  |  |
| OS       | Homo sapiens.  |  |
| XX       |  |  |
| FT       | Key  | Location/Qualifiers                                  |
| FT       | Domain   | 1..85  |
| FT       | Domain   | /note="epidermal growth factor-like domain 1"        |
| FT       | Domain   | 117..158   |
| FT       | Domain   | /note="epidermal growth factor-like domain 2"        |
| FT       | Domain   | 159..254   |
| FT       | Domain   | /note="domain HSM2 homologous to an HSMC3W5A domain" |
| XX       |  |  |
| PN       | MO9857983-A2.  |  |
| XX       |  |  |
| XX       |  |  |
| PD       | 23-DEC-1998.   |  |
| XX       |  |  |

PF 18-JUN-1998; 98WO-US12763.  
 XX 18-JUN-1997; 97US-0878322.  
 PR 18-JUN-1997; 97US-0050143.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;  
 PI Whitmore TE;  
 XX WPI; 1999-095324/08.  
 XX New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's  
 PT disease, cancer and to repopulate blood cells  
 XX Claim 6; Page 48-49; 70pp; English.  
 XX This polypeptide comprises human Zneul mature polypeptide. Zneul  
 CC is a new neuro-growth factor-like protein (see also AAW88381). Its  
 CC closest human homologue is HSMHC3W5A, a gene in the HLA class III  
 CC region, which is contained in a cosmid which contains Notch 4.  
 CC Zneul is also homologous to Notch 4 in its EGF-like domains and may  
 CC be involved in EGF receptor pathways. Zneul is widely expressed in  
 CC adult tissues, with high expression in heart, placenta, spleen,  
 CC testis, thyroid, spinal cord and lymph node. Zneul can be used as  
 CC a growth, maintenance, or differentiation factor in the spinal  
 CC cord, heart, spleen, testis, thyroid and lymph nodes. It may  
 CC play a role in breast cancer, glioblastomas, and pituitary  
 CC adenomas. Zneul may also be used to treat Alzheimer's disease,  
 CC cancer, to repopulate blood cells after chemotherapy, to stimulate  
 CC myofibroblast proliferation, stimulate or inhibit growth factors  
 CC made in the placenta, in fertility and contraception, or to  
 CC regenerate nerves. Claimed Zneul polypeptides (see also AAW88382-97),  
 CC including specific domains of Zneul and epitope-bearing portions of  
 CC Zneul, can be used to raise specific antibodies for use e.g. in  
 CC diagnostic assays.  
 XX Sequence 254 AA;  
 SQ  
 Query Match 100.0%; Score 1411; DB 20; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TEHAVRPGRRVCAVRAHGDVSESVQRYVQPLTTCGHRACSTYRTIYRTARRSPGL 60  
 Db 1 TEHAVRPGRRVCAVRAHGDVSESVQRYVQPLTTCGHRACSTYRTIYRTARRSPGL 60  
 QY 61 APARPRYACCPGWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTCCSDVD 120  
 Db 61 APARPRYACCPGWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTCCSDVD 120  
 QY 121 ECSARRGGCPQRCVNTAGSYWCQWEGHLSADGTLVCPKGGPPRVA NPFTGVDSAMKEE 180  
 Db 121 ECSARRGGCPQRCVNTAGSYWCQWEGHLSADGTLVCPKGGPPRVA NPFTGVDSAMKEE 180  
 QY 181 VQRLQSRVLLLEKQLVLAPHLASQALEHGLPDGSLVHVSFOQLGRIDLSLSEQISF 240  
 Db 181 VQRLQSRVLLLEKQLVLAPHLASQALEHGLPDGSLVHVSFOQLGRIDLSLSEQISF 240  
 QY 241 LEEQLGSCSKKDS 254  
 Db 241 LEEQLGSCSKKDS 254  
 RESULT 2  
 ID AAY41771 standard; Protein; 273 AA.  
 XX AAY41771;  
 AC AAY41771;  
 XX 07-DEC-1999 (first entry)  
 DT Human PRO1449 protein sequence.  
 XX DE

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 XX Homo sapiens.  
 OS WO9946281-A2.  
 PN 16-SEP-1999.  
 PD 08-MAR-1999;  
 PF 99WO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077649.  
 PR 12-MAR-1998; 98US-0077791.  
 PR 13-MAR-1998; 98US-0078004.  
 PR 17-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 20-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079294.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083322.  
 PR 29-APR-1998; 98US-0083392.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 29-APR-1998; 98US-0083559.  
 PR 30-APR-1998; 98US-0083742.  
 PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.



CC differentiation factor in the spinal cord, heart, spleen, testis,  
 CC thyroid and lymph nodes. It may also play a role in breast cancer,  
 CC glioblastomas, and pituitary adenomas. Zneul may be used to treat  
 CC Alzheimer's disease, cancer, to repopulate blood cells after  
 CC chemotherapy, to stimulate myofibroblast proliferation, stimulate  
 CC or inhibit growth factors made in the placenta, in fertility and  
 CC contraception, or to regenerate nerves. Claimed Zneul  
 CC polypeptides (see also AW89382-97), including specific domains of  
 CC Zneul and epitope-bearing portions of Zneul, can be used to raise  
 CC specific antibodies for use e.g. in diagnostic assays.

SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 20; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVRAGDPPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRVCAVRAGDPPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 79  
 QY 61 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGSGCVQPGRCRCPAGWRGDTCCSDVD 120  
 DB 80 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGSGCVQPGRCRCPAGWRGDTCCSDVD 139  
 QY 121 ECSARRGCGPCORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRPVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCGPCORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRPVAPNPTGVDSAMKEE 199  
 QY 181 VQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 240  
 DB 200 VQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 259  
 QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

## RESULT 4

AAB44327  
 ID AAB44327 standard; Protein; 273 AA.

XX AAB44327;

XX 08-FEB-2001 (first entry)

XX Human PRO1449 protein sequence SEQ ID NO:510.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.

XX Homo sapiens.

OS WO200053756-A2.

PN 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR

30-DEC-1999; 99WO-US31274.

PR

05-JAN-2000; 2000WO-US00219.

PR

06-JAN-2000; 2000WO-US00277.

XX

06-JAN-2000; 2000WO-US00376.

PA

(GETH) GENENTECH INC.

XX

Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI

Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI

Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI

Kl'javin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

PI

Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

XX

WPI; 2000-611443/58.

DR

N-PSDB; AAC78587.

XX

Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PT cellular activities -

XX

Claim 12; Fig 217; 636pp; English.

PS

XX

AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

XX

Sequence 273 AA;

SQ

Query Match 100.0%; Score 1411; DB 21; Length 273;

Best Local Similarity 100.0%; Pred. No. 3.5e-88;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TEHAYRPGRRVCAVRAGDPPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 60

DB

20 TEHAYRPGRRVCAVRAGDPPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 79

QY

61 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGSGCVQPGRCRCPAGWRGDTCCSDVD 120

DB

80 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGSGCVQPGRCRCPAGWRGDTCCSDVD 139

QY

121 ECSARRGCGPCORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRPVAPNPTGVDSAMKEE 180

DB

140 ECSARRGCGPCORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRPVAPNPTGVDSAMKEE 199

QY

181 VQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 240

DB

200 VQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 259

QY

241 LEEQLGSCCKKDS 254

DB

260 LEEQLGSCCKKDS 273

## RESULT 5

AAB18675

ID AAB18675 standard; Protein; 273 AA.

XX AAB18675;

AC AAB18675;

XX 22-JAN-2001 (first entry)

XX Amino acid sequence of a human a PRO1449 polypeptide.

DE Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO1449;

XX angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;

KW

XX endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
 XX arteriosclerosis; cardiac hypertrophy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Peptide 1..19  
 XX Modified-site /note= "signal sequence"  
 XX Modified-site 19..25  
 XX Modified-site /note= "N-myristoylation site"  
 XX Modified-site 26..30  
 XX Modified-site /note= "amidation site"  
 XX Modified-site 78..84  
 XX Modified-site /note= "N-myristoylation site"  
 XX Modified-site 93..97  
 XX /note= "CAMP- and GMP-dependent protein kinase  
 XX phosphorylation site"  
 XX Modified-site 97..103  
 XX /note= "N-myristoylation site"  
 XX Modified-site 100..106  
 XX /note= "N-myristoylation site"  
 XX Modified-site 103..109  
 XX /note= "N-myristoylation site"  
 XX Region 123..135  
 XX /note= "EGF-like domain cysteine pattern signature"  
 XX Region 130..133  
 XX /note= "cell attachment sequence"  
 XX Modified-site 152..164  
 XX /note= "aspartic acid and asparagine hydroxylation site"  
 XX Modified-site 157..163  
 XX /note= "N-myristoylation site"  
 XX Modified-site 191..197  
 XX /note= "N-myristoylation site"  
 XX Modified-site 265..271  
 XX /note= "N-myristoylation site"  
 XX WO200053752-A2.  
 XX 14-SEP-2000.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 21-APR-1999; 99US-0130232.  
 XX 26-APR-1999; 99US-0131022.  
 XX 28-APR-1999; 99US-0131445.  
 XX 14-MAY-1999; 99US-0134287.  
 XX 02-DEC-1999; 99WO-US28565.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM,  
 XX Wood WI,  
 XX WPI, 2000-638138/61.  
 XX N-PSDB; AAA5704.  
 XX A composition useful for treatment and diagnosis of a cardiovascular,  
 XX endothelial or angiogenic disorder, especially cancer, comprises (an  
 XX PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 XX PRO130 or PRO1449 polypeptide -  
 XX Claim 67; Fig 14; 152pp; English.  
 XX The present sequence represents PRO1449, a human notch 4 homologue.  
 XX The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,  
 XX PRO130 and PRO1449 polypeptides. The polypeptides promote or  
 XX inhibit angiogenesis and cardiovascularisation in mammals. The  
 XX polypeptides are used for the treatment and diagnosis of a  
 XX cardiovascular, endothelial or angiogenic disorder, especially  
 XX cancer. Disorders that can be diagnosed, treated or prevented by  
 XX the polypeptides of the invention include trauma such as wounds,  
 XX arteriosclerosis, and cardiac hypertrophy.

XX SQ Sequence 273 AA;  
 XX Query Match 100.0%; Score 1411; DB 21; Length 273;  
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TEHAYRPRRYCAVAHAGDPVSESFVORVYOPPLTTCDGHRACSTYRTIYRTAYRSPGL 60  
 DB 20 TEHAYRPRRYCAVAHAGDPVSESFVORVYOPPLTTCDGHRACSTYRTIYRTAYRSPGL 79  
 QY 61 APARPRRYACCPGWRKTSGLPACGAAITQPPCRNGSGCVOPRCRCPAKMGRTCCSDVD 120  
 DB 80 APARPRRYACCPGWRKTSGLPACGAAITQPPCRNGSGCVOPRCRCPAKMGRTCCSDVD 139  
 QY 121 EGSARRGGCPORCVNTAGSYWCOCMEGHSLSADGTLCPKGGPRVA PNPYGVDSAMKEE 180  
 DB 140 EGSARRGGCPORCVNTAGSYWCOCMEGHSLSADGTLCPKGGPRVA PNPYGVDSAMKEE 199  
 QY 181 VORLQSRVDLLEEKQLQVLAFLHSLASQALEHGLPDPGSLVHSPQOLGRIDSLSQISF 240  
 DB 200 VORLQSRVDLLEEKQLQVLAFLHSLASQALEHGLPDPGSLVHSPQOLGRIDSLSQISF 259  
 QY 241 LEEQLGSCSCCKDS 254  
 DB 260 LEEQLGSCSCCKDS 273  
 XX RESULT 6  
 XX AAB24044  
 XX ID AAB24044 standard; Protein; 273 AA.  
 XX AC AAB24044;  
 XX XX 25-JAN-2001 (first entry)  
 XX DE Human PRO1449 protein sequence SEQ ID NO:8.  
 XX KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
 XX tumorigenesis; detection; neoplastic cell growth; proliferation;  
 XX cytostatic; anti-inflammatory; immunomodulatory; inflammatory disorder;  
 XX immunological disorder.  
 XX OS Homo sapiens.  
 XX PN WO200053754-A1.  
 XX 14-SEP-2000.  
 XX 06-JAN-2000; 2000WO-US00277.  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 12-MAR-1999; 99US-0123957.  
 XX 29-MAR-1999; 99US-0126773.  
 XX 21-APR-1999; 99US-0130232.  
 XX 28-APR-1999; 99US-0131445.  
 XX 05-OCT-1999; 99WO-US23089.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 02-DEC-1999; 99WO-US28561.  
 XX 02-DEC-1999; 99WO-US28564.  
 XX 30-DEC-1999; 99WO-US31243.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA,  
 XX Wood WI,  
 XX WPI, 2000-572269/53.  
 XX N-PSDB; AAC58228.  
 XX New isolated antibody for use in compositions and methods for the  
 XX diagnosis and treatment of neoplastic cell growth and proliferation in

PT mammals, including humans, and in monitoring tumor treatment -

PS Claim 61; Fig 8; 195pp; English.

XX The present invention describes an isolated antibody (Ab) that binds to  
 CC one of the human proteins (P) designated PRO1330, PRO1449,  
 CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO538, PRO3664, PRO618,  
 CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions  
 CC and methods for the diagnosis and treatment of neoplastic cell growth  
 CC and proliferation in mammals, including humans. Genes and polypeptides  
 CC encoded by them, that are amplified in the genome of a tumour cell, can  
 CC be identified and are useful targets for the treatment and prevention of  
 CC certain cancers and may be used to monitor tumour treatment. Compounds  
 CC that inhibit the expression or activity of the identified polypeptides  
 CC can be identified and used as antagonists. Benign or malignant tumours,  
 CC inflammatory disorders and immunological disorders can be treated.  
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
 CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 21; Length 273;

Best Local Similarity 100.0%; Pred. No. 3.5e-88;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEHAYRFGRRVCAVRAHGDVPVSEFVQVQPFLLTCDGHRACSTYRTIYTRRSPGL 60

Db 20 TEHAYRFGRRVCAVRAHGDVPVSEFVQVQPFLLTCDGHRACSTYRTIYTRRSPGL 79

Qy 61 APAPRYACCGWRTSGLPACAAACOPPCRNCGSCVQPCRCRCAGWGTCCSDVD 120

Db 80 APAPRYACCGWRTSGLPACAAACOPPCRNCGSCVQPCRCRCAGWGTCCSDVD 139

Qy 121 ECSARRGCPORCVNTAGSVCQWEGHLSADGTLCPKGGPPRVAPNPTGVDSAMKEE 180

Db 140 ECSARRGCPORCVNTAGSVCQWEGHLSADGTLCPKGGPPRVAPNPTGVDSAMKEE 199

Qy 181 VORLQSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 240

Db 200 VORLQSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 259

Qy 241 LEEOLGSCSCKKDS 254

Db 260 LEEOLGSCSCKKDS 273

RESULT 7

AAB01376

ID AAB01376 standard; Protein; 273 AA.

XX AAB01376;

XX 20-OCT-2000 (first entry)

XX Neuron-associated protein.

XX Neuron associated protein; NEUAP; neurological disorder; epilepsy;  
 KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;  
 KW Alzheimer's disease; Pick's disease; Huntington's disease;  
 KW dementia; Parkinson's disease; demyelinating disease; meningitis;  
 KW cerebral palsy; muscular dystrophy; central nervous system; CNS;  
 KW peripheral nervous system; PNS; myopathy; schizophrenia;  
 KW actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;  
 KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;  
 KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;  
 KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;  
 KW AIDS; Addison's disease; adult respiratory distress syndrome;  
 KW allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;  
 KW werner syndrome, trauma; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Modified-site 54 /label= Signal peptide

FT Modified-site 64 /note= "Potential phosphorylation site"

FT Modified-site 96 /note= "Potential phosphorylation site"

FT Domain 107..134 /note= "Potential phosphorylation site"

FT Region 130..132 /label= EGF-like domain

FT Modified-site 136 /label= Cell attachment sequence

FT Domain 141..176 /note= "Potential phosphorylation site"

FT Modified-site 142 /label= EGF-like domain

FT Modified-site 152..163 /note= "Potential phosphorylation site"

FT Modified-site 190 /label= Asx hydroxylation site

FT Modified-site 205 /note= "Potential phosphorylation site"

FT Modified-site 252 /note= "Potential phosphorylation site"

FT Modified-site 258 /note= "Potential phosphorylation site"

FT Modified-site 268 /note= "Potential phosphorylation site"

FT Modified-site 273 /note= "Potential phosphorylation site"

XX WO200034477-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99WO-US30408.

XX 11-DEC-1998; 98US-0210083.

XX 11-DEC-1998; 98US-9123456.

XX 09-FEB-1999; 99US-0119365.

XX 16-MAR-1999; 99US-0124687.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;

XX Lu DAM, Azimzal Y;

XX WPI; 2000-423423/36.

XX N-PSDB; AAA47417.

XX New human neuron-associated proteins and polynucleotides encoding them,  
 XX useful for diagnosis, treatment and prevention of cell proliferative  
 XX disorders including cancer, neuronal and neurological disorders  
 XX Claim 1; Page 97; 145pp; English.

XX Human neuron-associated proteins (NEUAP) can be used for  
 XX treating or preventing a disorder associated with decreased  
 XX expression or activity of NEUAP. Antagonists of NEUAP are useful for  
 XX treating or preventing disorder associated with increased expression  
 XX or activity of NEUAP. NEUAP or their fragments or derivatives are  
 XX useful for treating neurological disorder such as epilepsy, ischemic  
 XX cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's  
 XX disease, Pick's disease, Huntington's disease, dementia and  
 XX Parkinson's disease. NEUAPs are also useful for treating other  
 XX demyelinating diseases, bacterial and viral meningitis, prion  
 XX diseases including kuru, Creutzfeldt-Jakob disease, nutritional and  
 XX metabolic diseases of the nervous system, neurofibromatosis, other



CC developmental disorders of the central nervous system, cerebral  
CC palsy, neurokalethal disorders, autonomic nervous system disorders,  
CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and  
CC other neuromuscular disorders, peripheral nervous system disorders,  
CC inherited, metabolic, endocrine, and toxic myopathies, mental  
CC disorders including mood, anxiety and schizoprenic disorders, a cell  
CC proliferative disorder such as actinic keratosis, arteriosclerosis,  
CC atherosclerosis, busitis, cirrhosis, hepatitis, mixed connective  
CC tissue disease (MCTD), myofibrosis, paroxysmal nocturnal  
CC haemoglobinuria, cancers of the adrenal gland, bladder, bone,  
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory  
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's  
CC disease, adult respiratory distress syndrome, allergies, ankylosing  
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,  
CC complications of cancer, hemodialysis, and extracorporeal circulation,  
CC viral, bacterial, fungal parasitic, protozoal, and helminthic  
CC infections, and trauma. This protein was given the Incey ID no.  
829443CDL.

XX

Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 21; Length 273;  
Bert Local Similarity 100.0%; Pred. No. 3.5e-86;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**SQ**      **Sequence**      **273 AA;**

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 1411;        | DB 21;    | Length 273; |
| Best Local Similarity | 100.0%;         | Pred. No. 3.5e-88; |           |             |
| Matches 254;          | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;     |

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | TEHAYRPFARFACARAGDPVSEFVQVVOPELTTCDDGRACSTYTRTAYRSPGL        | 60  |
| Db | 20  | TEHAYRPFARFACARAGDPVSEFVQVVOPELTTCDDGRACSTYTRTAYRSPGL        | 79  |
| QY | 61  | APAPBRVACPCGKMTSGLPAGCAAIQCPCCRNQSSCVQPGRCPCPAGRGDTQSDVD     | 120 |
| Db | 80  | APAPBRVACPCGKMTSGLPAGCAAIQCPCCRNQSSCVQPGRCPCPAGRGDTQSDVD     | 139 |
| QY | 121 | EC SARGGCCPCRCVNTGSSVYCOCMBEHSLSADDTLCVPKGGPBRVAPNPTGVDSAMKE | 180 |
| Db | 140 | EC SARGGCCPCRCVNTGSSVYCOCMBEHSLSADDTLCVPKGGPBRVAPNPTGVDSAMKE | 199 |
| QY | 181 | VQRLQSRVDLLEKTLQVLAPRLHSLASQALEHGLPDEGSLLVHFSFOQLGRIDLSIQISF | 240 |
| Db | 200 | VQRLQSRVDLLEKTLQVLAPRLHSLASQALEHGLPDEGSLLVHFSFOQLGRIDLSIQISF | 259 |
| QY | 241 | LEBQLGSCSCCKDS   | 254 |
| Db | 260 | LEBQLGSCSCCKDS   | 273 |

## RESULT 8

|    |          |                            |
|----|----------|----------------------------|
| ID | AAM23991 | standard; protein; 273 AA. |
|----|----------|----------------------------|

|    |                           |
|----|---------------------------|
| AC | AAM23991;                 |
| XX |                           |
| DT | 12-OCT-2001 (first entry) |
| xx |                           |

Human EST encoded protein SEQ ID NO: 1516.

KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; KM diagnostics; forensic test; gene mapping; genetic disorder; KM biodiversity; gene therapy; nutrition.

OS Homo sapiens

PN WO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02687.  
XY

PR 25-JAN-2000; 2000US-0491404.  
PB 17-JUL-2000; 2000US-0617746

PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0653970

XX (HYSE-) HYSEQ INC.  
PA

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX  
WBT : 3003-476164/67  
DB

DR N-PSDB; AAH98650.  
XY

PT Isolated polypeptide  
PT antibodies and resea

PS Claim 20: Page 1046-1047: 1275pm: English  
XX

CC The present invention provides

CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention.

SQ Sequence 273 AA;

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 100.0%         | Score 1411        | DB 22    | Length 273 |
| Best Local Similarity | 100.0%         | Pred. No. 3.5e-88 |          |            |
| Matches 254           | Conservative 0 | Mismatches 0      | Indels 0 | Gaps 0     |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | TEHAAYPGRRVAVAAHMDPVSESFVQRYVQPLTTCDGHRACSTYRITVTYARSPGL      | 60  |
| Db | 20  | TEHAAYPGRRVAVAAHMDPVSESFVQRYVQPLTTCDGHRACSTYRITVTYARSPGL      | 79  |
| Qy | 61  | APARPRVYACCEMKRTSGLPACGAALCPDPCNGGSCVQPRCRCPAGMRDTCQDVD       | 120 |
| Db | 80  | APARPRVYACCEMKRTSGLPACGAALCPDPCNGGSCVQPRCRCPAGMRDTCQDVD       | 139 |
| Qy | 121 | ECGARGGGPOPCVNTAGSYVCCQMEGHSLSADGTLCVKGGPRPVAAINPPIGVSNAAKEE  | 180 |
| Db | 140 | ECGARGGGCPQCVNTAGSYVCCQMEGHSLSADGTLCVKGGPRPVAAINPPIGVDSAAKEE  | 199 |
| Qy | 181 | VQRLQSRVDLLEBKQLQVLVADLHSLASQALEHGLPDPGSLVHVSFOQLGRIDLSLEQISF | 240 |
| Db | 200 | VQRLQSRVDLLEBKQLQVLVADLHSLASQALEHGLPDPGSLVHVSFOQLGRIDLSLEQISF | 259 |
| Qy | 241 | LEEQLGSGSCCKKDS   | 254 |
| Db | 260 | LEEQLGSGSCCKKDS   | 273 |

## RESULT 9

| ID       | standard; Protein; 273 AA. |
|----------|----------------------------|
| AA061609 |                            |

AC AAB61609;  
yy

|    |             |               |
|----|-------------|---------------|
| DT | 05-APR-2001 | (first entry) |
| YY |             |               |

DE Human protein HP033375.  
XX

KM Humair; hydrophobic domain; immune deficiency; autoimmune disorder;  
KM allergy; tissue growth; regeneration; wound healing; burn; tumour;  
KM periodontal disease; thrombolytic condition; haemostatic condition;  
KM infection.

OS Homo sapiens.  
XY

PN WO200102563-A2  
XX

PD 11-JAN-2001  
XX

PF 16-JUN-2000; 2000WO-JP03943.  
XX







PT to target bioactive molecules to specific cells, and to modulate  
PT cellular activities -  
XX  
XX Claim 12, Fig 213, 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.

XX Sequence 273 AA;

Query Match 99.9%; Score 1410; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred. No. 4.1e-88;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHAGDPVSESFVQRYOPFLTTCCGHRACSTYRTTYTAYRRSPGL 60  
DB 20 TEHAYRPGRRVCAVAHAGDPVSESFVQRYOPFLTTCCGHRACSTYRTTYTAYRRSPGL 79  
QY 61 APARPRVACCPGMRKRTSGLPACGAATCOPPCRNAGSCVQPGRCRCPAGMRGDTQSDVD 120  
DB 80 APARPRVACCPGMRKRTSGLPACGAATCOPPCRNAGSCVQPGRCRCPAGMRGDTQSDVD 139  
QY 121 ECSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRVANPTGVDSAMKEE 180  
DB 140 ECSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRVANPTGVDSAMKEE 199  
QY 181 VORLOSRVDLLEKQLQVLAHPLHSLASQALEHGLPDPGSLLVHSPQUGRIDSLSEQISF 240  
DB 200 VORLOSRVDLLEKQLQVLAHPLHSLASQALEHGLPDPGSLLVHSPQUGRIDSLSEQISF 259  
QY 241 LEEQLGSCCKKDS 254  
DB 260 LEEQLGSCCKKDS 273

RESULT 13

AAB44326 AAB44326 standard; Protein; 273 AA.

XX AAB44326;

XX 08-FEB-2001 (first entry)

XX Human PRO1330 protein sequence SEQ ID NO:508.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;

XX expressed sequence tag; detection; cancer.

OS Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 29-MAR-1999; 99US-0126773.

XX 21-APR-1999; 99US-0130232.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 23-JUN-1999; 99US-0141037.

XX 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28351.  
PR 02-DEC-1999; 99WO-US28351.  
PR 16-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.

XX (GENTH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Periera N, Filvaroff E, Fong S, Gao W, Garber H, Gertsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kijavini IU, Kuo SS, Napier MA, Pan J, Peoni NF, Roy MA;  
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX MPI; 2000-611443/58.  
XX N-PSDB; AAC78586.

PT Novel PRO polypeptides and polynucleotides used in detection methods,  
PT to target bioactive molecules to specific cells, and to modulate  
PT cellular activities -

XX Claim 12, Fig 215, 636pp; English.

CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.

XX Sequence 273 AA;

Query Match 99.9%; Score 1410; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred. No. 4.1e-88;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHAGDPVSESFVQRYOPFLTTCCGHRACSTYRTTYTAYRRSPGL 60  
DB 20 TEHAYRPGRRVCAVAHAGDPVSESFVQRYOPFLTTCCGHRACSTYRTTYTAYRRSPGL 79  
QY 61 APARPRVACCPGMRKRTSGLPACGAATCOPPCRNAGSCVQPGRCRCPAGMRGDTQSDVD 120  
DB 80 APARPRVACCPGMRKRTSGLPACGAATCOPPCRNAGSCVQPGRCRCPAGMRGDTQSDVD 139  
QY 121 ECSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRVANPTGVDSAMKEE 180  
DB 140 ECSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRVANPTGVDSAMKEE 199  
QY 181 VORLOSRVDLLEKQLQVLAHPLHSLASQALEHGLPDPGSLLVHSPQUGRIDSLSEQISF 240  
DB 200 VORLOSRVDLLEKQLQVLAHPLHSLASQALEHGLPDPGSLLVHSPQUGRIDSLSEQISF 259  
QY 241 LEEQLGSCCKKDS 254  
DB 260 LEEQLGSCCKKDS 273

RESULT 14

AAB18673 AAB18673 standard; Protein; 273 AA.

XX AAB18673;



Search completed: December 17, 2002, 10:01:34  
Job time : 31.3643 secs

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FT Modified-site 152..164
FT /note= "aspartic acid and asparagine hydroxylation site"
FT Modified-site 157..163
FT /note= "N-myristoylation site"
FT Modified-site 191..197
FT /note= "N-myristoylation site"
FT Modified-site 265..271
FT /note= "N-myristoylation site"
XX
XX WO200053752-A2.
XX
XX 14-SEP-2000.
XX
XX 30-DEC-1999; 99WO-US31274.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 21-APR-1999; 99US-0130232.
XX 26-APR-1999; 99US-0131022.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 02-DEC-1999; 99WO-US28565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM,
XX Wood WI;
XX
XX WPI; 2000-638138/61.
XX
XX N-PSDB; AAA75703.
XX
XX A composition useful for treatment and diagnosis of a cardiovascular,
XX endothelial or angiogenic disorder, especially cancer, comprises (an
XX agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,
XX PRO1330 or PRO1449 polypeptide -
XX
XX
XX Claim 67; Fig 12; 152pp; English.
XX
XX
XX The present sequence represents PRO1330, a human notch 4 homologue.
XX The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,
XX PRO1330 and PRO1449 polypeptides. The polypeptides promoter or
XX inhibit angiogenesis and cardiovascularisation in mammals. The
XX polypeptides are used for the treatment and diagnosis of a
XX cardiovascular, endothelial or angiogenic disorder, especially
XX cancer. Disorders that can be diagnosed, treated or prevented by
XX the polypeptides of the invention include trauma such as wounds,
XX atherosclerosis, and cardiac hypertrophy.
XX
XX
XX Sequence 273 AA;
XX
XX
XX Query Match 99.9%; Score 1410; DB 21; Length 273;
XX Best Local Similarity 99.6%; Pred. No. 4..1e-88;
XX Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TEHAYRGRRCVCAVRAGDPVSEFVQRYVQPLTTCDGHRACSTYRTTTRTAIRSPGL 60
XX |
XX |
XX |
XX 20 TEHAYRGRRCVCAVRAGDPVSEFVQRYVQPLTTCDGHRACSTYRTTTRTAIRSPGL 79
XX |
XX |
XX |
XX 61 APAPRYACCPGMRRTISGLPGACGAICOPPCRNAGSCVOPGRCRCPAGRGDTCOSDVD 120
XX |
XX |
XX |
XX 80 APAPRYACCPGMRRTISGLPGACGAICOPPCRNAGSCVOPGRCRCPAGRGDTCOSDVD 139
XX |
XX |
XX |
XX QY 121 ECSARRGGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRYVAPNPTGVDSAMKEE 180
XX |
XX |
XX |
XX 140 ECSARRGGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRYVAPNPTGVDSAMKEE 199
XX |
XX |
XX |
XX QY 181 VQRLQSRVDLLEKTLQVLAPLHSLASOALEHGLPDRGSLVHSFOQLGRIDSLEQISF 240
XX |
XX |
XX |
XX DB 200 VQRLQSRVDLLEKTLQVLAPLHSLASOALEHGLPDRGSLVHSFOQLGRIDSLEQISF 259
XX |
XX |
XX |
XX QY 241 LEEQLGSCSCCKDS 254
XX |
XX |
XX |
XX DB 260 LEEQLGSCSCCKDS 273
XX |
XX |
XX |
```







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Db      2  PLPWSIALPULLLPWVAGGFGNAASARHHGLASA--RQPGVCHVTGTLKACYGWRNS--  57
QY      80  PGACGAAICQPPCRNGGSCVQPRCPCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGS  139
Db      58  KGVC-EATCEPGCK-FGECVGNKCRCPFGYGTGKTCSDQVNECGMKPRPCQHRVCVNTGHS  115
QY      140  YWCQCWEHSLSADGTLCV-----PKGPP-----RVAPN  169
Db      116  YKFCFLSGHMLPDAT-CVNSRTCAMINCOYSCDTEEGPQCLCPSSGLRLAPN  168

RESULT 4
US-09-249-697A-19
; Sequence 19, Application US/09249697A
; Patent No. 6392018
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
; TITLE OF INVENTION: LIVER SPLEEN
; FILE REFERENCE: 24011-727
; CURRENT APPLICATION NUMBER: US/09/249,697A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-249-697A-19

Query Match      17.9%; Score 252.5; DB 4; Length 553;
Best Local Similarity 37.4%; Pred. No. 1.6e-12;
Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;

QY      39  GHRACSTYRTIVRTAYRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSC  98
Db      21  GNAASARHHGLASA--RQPGVCHVTGTLKACYGWRNS--KGVC-EATCEPGCK-FGEC  74
QY      99  VQPRCPCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCQCWEHSLSADGTLCV  158
Db      75  VGNKCRCPFGYGTGKTCSDQVNECGMKPRPCQHRVCVNTGHSYKFCFLSGHMLPDAT-CV  133
QY      159  -----PKGPP-----RVAPN  169
Db      134  NSRTCAMINCOYSCDTEEGPQCLCPSSGLRLAPN  168

RESULT 5
US-09-363-316B-24
; Sequence 24, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-363-316B-24

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| Query Match | Best Local Similarity                                 | Score | DB 4      | Length | DB 4        | Length | DB 4 | Length |
|-------------|---|-------|-----------|--------|-------------|--------|------|--------|
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 134         | ASGRQCSCPEGTGEOQLRDFCSA                               | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 117         | SDVDECSARRGGCPQ--RCVNTAGSYWCQC                        | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 190         | RUINECFLEPGPCPGTSGHNTLSYQCLCPVQGGQKLRKGCACPPGSLNGTCLV | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 168         | PNP-----TGVDAMKEE                                     | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 250         | PEGHSTFHLCLCPGFTGLDCEMNP                              | 13.9% | Score 196 | DB 4   | Length 1964 |        |      |        |
| 61          | APARYACCPGK--RTSLPGACGAACQPPCRNGSGCVOPG               | 13.9% | Score 196 | DB 4   |             |        |      |        |

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPLTTCGH-----RACSTYRTYRTAYRSPGLAPRPRVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLECEVELCS--REARVFEVNDPETYPRYLDCKNKYGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQP--GR--CRCPAGMRGDTQGSVDDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNEC 160  
QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLC 157  
DB 161 SQENGGCLQICHNKPGSFHCSGHSFELSSDGRTC 195

## RESULT 13

US-08-435-434-2  
Sequence 2, Application US/08435434  
Patent No. 5714385

GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHMANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,434  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-434-2

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPLTTCGH-----RACSTYRTYRTAYRSPGLAPRPRVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLECEVELCS--REARVFEVNDPETYPRYLDCKNKYGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQP--GR--CRCPAGMRGDTQGSVDDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNEC 160

QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLC 157  
DB 161 SQENGGCLQICHNKPGSFHCSGHSFELSSDGRTC 195

## RESULT 14

US-08-435-436-2  
Sequence 2, Application US/08435436  
Patent No. 5721139

GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHMANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,436  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-436-2

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPLTTCGH-----RACSTYRTYRTAYRSPGLAPRPRVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLECEVELCS--REARVFEVNDPETYPRYLDCKNKYGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQP--GR--CRCPAGMRGDTQGSVDDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFFCLCKAGWGRLCDKDVNEC 160  
QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLC 157  
DB 161 SQENGGCLQICHNKPGSFHCSGHSFELSSDGRTC 195

## RESULT 15

US-08-438-863-2  
Sequence 2, Application US/08438863  
Patent No. 5849585

GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Ronghao Li

Search completed: December 17, 2002, 10:04:12  
Job time : 14.5313 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 10:03:07 ; Search time 8.19355 Seconds  
(without alignments)  
516.533 Million cell updates/sec

Title: US-09-852-472-3  
Perfect score: 1411  
Sequence: 1 TEHAYRPGRRVCVAVRAGDP.....SEQSFLREUUGSCSCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues  
Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCF\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID                 | Description       |
|------------|--------|-------------|--------|--------------------|-------------------|
| 1          | 1411   | 100.0       | 273    | US-09-978-295A-510 | Sequence 510, App |
| 2          | 1411   | 100.0       | 273    | US-09-978-697-510  | Sequence 510, App |
| 3          | 1411   | 100.0       | 273    | US-09-978-192A-510 | Sequence 510, App |
| 4          | 1410   | 99.9        | 273    | US-09-978-295A-506 | Sequence 506, App |
| 5          | 1410   | 99.9        | 273    | US-09-978-295A-508 | Sequence 508, App |
| 6          | 1410   | 99.9        | 273    | US-09-978-697-506  | Sequence 506, App |
| 7          | 1410   | 99.9        | 273    | US-09-978-697-508  | Sequence 508, App |
| 8          | 1410   | 99.9        | 273    | US-09-978-192A-506 | Sequence 506, App |
| 9          | 1410   | 99.9        | 273    | US-09-978-192A-508 | Sequence 508, App |
| 10         | 1410   | 99.9        | 273    | US-09-978-295A-510 | Sequence 510, App |
| 11         | 1392   | 96.7        | 251    | US-09-790-264-10   | Sequence 10, Appl |
| 12         | 1333   | 94.5        | 295    | US-09-978-295A-2   | Sequence 12, Appl |
| 13         | 1333   | 94.5        | 295    | US-09-978-697-2    | Sequence 2, Appl1 |
| 14         | 1333   | 94.5        | 295    | US-09-978-192A-2   | Sequence 2, Appl1 |
| 15         | 1139.5 | 80.8        | 275    | US-09-790-264-15   | Sequence 15, Appl |
| 16         | 945.5  | 67.0        | 287    | US-09-764-898-218  | Sequence 218, App |
| 17         | 945.5  | 67.0        | 288    | US-09-764-853-841  | Sequence 841, App |
| 18         | 945.5  | 67.0        | 288    | US-09-764-898-290  | Sequence 290, App |
| 19         | 945.5  | 67.0        | 314    | US-09-764-853-670  | Sequence 670, App |

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| 20 | 919.5 | 65.2 | 247  | 10 | US-09-790-264-20   | Sequence 20, Appl  |
| 21 | 255.5 | 18.1 | 553  | 9  | US-09-981-649A-6   | Sequence 6, Appl1  |
| 22 | 252.5 | 17.9 | 338  | 9  | US-09-978-295A-119 | Sequence 119, Appl |
| 23 | 252.5 | 17.9 | 338  | 9  | US-09-978-697-119  | Sequence 119, Appl |
| 24 | 252.5 | 17.9 | 338  | 9  | US-09-978-192A-119 | Sequence 119, Appl |
| 25 | 252.5 | 17.9 | 553  | 10 | US-09-981-649A-24  | Sequence 24, Appl  |
| 26 | 252.5 | 17.9 | 554  | 10 | US-09-981-649A-32  | Sequence 32, Appl  |
| 27 | 250.5 | 17.8 | 554  | 10 | US-09-981-649A-10  | Sequence 30, Appl  |
| 28 | 250.5 | 17.8 | 559  | 9  | US-09-981-649A-28  | Sequence 28, Appl  |
| 29 | 223   | 15.8 | 509  | 9  | US-09-905-291A-315 | Sequence 315, App  |
| 30 | 223   | 15.8 | 509  | 10 | US-09-909-320-315  | Sequence 315, App  |
| 31 | 223   | 15.8 | 509  | 10 | US-09-909-088B-315 | Sequence 315, App  |
| 32 | 223   | 15.8 | 509  | 12 | US-10-052-586-52   | Sequence 32, Appl  |
| 33 | 217.5 | 15.4 | 502  | 10 | US-09-981-649A-18  | Sequence 18, Appl  |
| 34 | 217.5 | 15.4 | 537  | 10 | US-09-981-649A-4   | Sequence 4, Appl1  |
| 35 | 216.5 | 15.3 | 100  | 10 | US-09-981-649A-3   | Sequence 3, Appl1  |
| 36 | 207   | 14.7 | 201  | 10 | US-09-764-853-797  | Sequence 797, App  |
| 37 | 207   | 14.7 | 201  | 10 | US-09-764-898-270  | Sequence 270, App  |
| 38 | 184   | 13.0 | 652  | 10 | US-09-789-919-96   | Sequence 96, Appl  |
| 39 | 183   | 13.0 | 810  | 10 | US-09-976-165-34   | Sequence 34, Appl  |
| 40 | 181.5 | 12.9 | 816  | 10 | US-09-976-165-37   | Sequence 37, Appl  |
| 41 | 173.5 | 12.3 | 1246 | 10 | US-09-919-497-85   | Sequence 85, Appl  |
| 42 | 172   | 12.2 | 534  | 10 | US-09-804-156-14   | Sequence 14, Appl  |
| 43 | 172   | 12.2 | 534  | 10 | US-09-946-633-6    | Sequence 6, Appl1  |
| 44 | 169   | 12.0 | 1055 | 10 | US-09-855-722-2    | Sequence 2, Appl1  |
| 45 | 166   | 11.8 | 1212 | 10 | US-09-855-722-3    | Sequence 3, Appl1  |

ALIGNMENTS

RESULT 1  
US-09-978-295A-510  
Sequence 510, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillman, Kenneth J.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P11  
CURRENT APPLICATION NUMBER: US/09/978, 295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249

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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1411; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 7, 8e-94;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 APAPRRACCPGMRGTGSLGAGCAALCOPPCRNCGSCVQPCRCPCAGKRGPTCCSDVD 120  
DB 80 APAPRRACCPGMRGTGSLGAGCAALCOPPCRNCGSCVQPCRCPCAGKRGPTCCSDVD 139

QY 121 ECSARRGCGQRCVNTAGSYWCQCEGHSLSADDTLCVPKGGPPRVAPNPTGVDSAMKEE 180  
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QY 181 VORIQSVLDLEELQLVLAPLHSLASQALEHGLPDGSLLVHSPQGLRIDSLSQISF 240  
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QY 241 LEBQLGSCGCKXS 254  
DB 260 LEBQLGSCGCKXS 273

RESULT 2  
US-09-978-697-510  
Sequence 510, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Snelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978, 697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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| 23 | PRIOR FILING DATE: 1998-04-22       |  |
| 24 | PRIOR APPLICATION NUMBER: 60/082804 |  |
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| 46 | PRIOR APPLICATION NUMBER: 60/083554 |  |
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| 67 | PRIOR FILING DATE: 1998-05-07       |  |
| 68 | PRIOR APPLICATION NUMBER: 60/084640 |  |
| 69 | PRIOR FILING DATE: 1998-05-07       |  |
| 70 | PRIOR APPLICATION NUMBER: 60/084598 |  |
| 71 | PRIOR FILING DATE: 1998-05-07       |  |
| 72 | PRIOR APPLICATION NUMBER: 60/084600 |  |
| 73 | PRIOR FILING DATE: 1998-5-07        |  |
| 74 | PRIOR APPLICATION NUMBER: 60/084627 |  |
| 75 | PRIOR FILING DATE: 1998-05-07       |  |

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|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/084643  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-07 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085339  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-13 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085338  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-13 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085323  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-13 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085582  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085700  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085689  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085579  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085580  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085573  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085704  |  |
|    | /  | PRIOR FILING DATE:   | 1998-05-15 |  |
|    | /  | PRIOR APPLICATION NUMBER:                                      | 60/085697  |  |
|    | Query Match            100.0%; Score 1411; DB 9; Length 273;                                 |  |            |  |
|    | Best Local Similarity     100.0% ; Pred. No. 7, 8e-94;                                       |  |            |  |
|    | Matches       254; Conservative          0; Mismatches      0; Indels       0; Gaps       0; |  |            |  |
| Qy | 1  | TEHAYRPGREVCVRAHGDDPVSESFVQRVVYQPFLTTCDGHRACSTYTETIYRTAYRRSPGL | 60         |  |
| Dd | 20   | TEHAYRPGREVCVRAHGDDPVSESFVQRVVYQPFLTTCDGHRACSTYTETIYRTAYRRSPGL | 79         |  |
| Qy | 61   | APARPRVACCPCGWKRTISLGPAGCAATCQQPCRNGSGCVOPGRCCRPAGWRGTTCQSDVD  | 120        |  |
| Dd | 80   | APARPRVACCPCGWKRTISLGPAGCAALCPQCRNCGSCVPQRCRCFPAGRGDTTCQSDVD   | 139        |  |
| Qy | 121  | ECSARRGGCPQRCVNNTAGSVWCOCWEHSLSADGTLCPVKGGPPRVAPNPMTGVDSAMKEE  | 180        |  |
| Dd | 140  | ECSARRGGCPQRCVNNTAGSVWCOCWEHSLSADGTLCPVKGGPPRVAPNPMTGVDSAMKEE  | 199        |  |
| Qy | 181  | VORIQSVRDILLEKLQVLVALPHLSASQAELHPDPGSLLVHSFQQLGRIDSLSEQISP     | 240        |  |
| Dd | 200  | VORIQSVRDILLEKLQVLVALPHLSASQAELHPDGESLLVHSFQQLGRIDSLSEQISP     | 259        |  |
| Qy | 241  | LEEOLGSCCKKDSS   | 254        |  |
| b  | 260  | LEEOLGSCCKKDS  | 273        |  |

### RESULT 3

US-09-978-192A-510  
Sequence 510, Application US/09978192A  
Patent No. US2002017753A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
PRIOR APPLICATION NUMBER: 2001-10-15  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
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PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639

Tue Dec 17 14:03:55 2002

PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1411; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 7.8e-94;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TEHAYRGRVCAVRAHGDVPSVSVFVORVYQPELTTCDDHRACTVTRTYRTAYRRSPGL 60  
20 TEHAYRGRVCAVRAHGDVPSVSVFVORVYQPELTTCDDHRACTVTRTYRTAYRRSPGL 79  
61 APAPRVAACPGWKTGSLPGACCAATCQPPCRNGSCVQPGRCPCAGWRGDTCSQVD 120  
80 APAPRVAACPGWKTGSLPGACCAATCQPPCRNGSCVQPGRCPCAGWRGDTCSQVD 139  
121 ECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPKGGPPRVAPNPTGVDSAMKEE 180  
140 ECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCPKGGPPRVAPNPTGVDSAMKEE 199  
181 VORLOSVDLLEKQLVLAPLHSLASQALEHGLPFGSLLVHVSFOQLGRIDSLSEQISF 240  
200 VORLOSVDLLEKQLVLAPLHSLASQALEHGLPFGSLLVHVSFOQLGRIDSLSEQISF 259  
241 LEEQLGSCSKKXDS 254  
260 LEEQLGSCSKKXDS 273

RESULT 4  
US-09-978-295A-506  
Sequence 506, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritson, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Faoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC11  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107

; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080165  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080194  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080327  
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 ; PRIOR APPLICATION NUMBER: 60/080328  
 ; PRIOR FILING DATE: 1998-04-01  
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 ; PRIOR FILING DATE: 1998-04-08  
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 ; PRIOR APPLICATION NUMBER: 60/081071  
 ; PRIOR FILING DATE: 1998-04-08  
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 ; PRIOR APPLICATION NUMBER: 60/081838  
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 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082804  
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 ; PRIOR APPLICATION NUMBER: 60/082700  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082797  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082796  
 ; PRIOR FILING DATE: 1998-04-23  
 ; PRIOR APPLICATION NUMBER: 60/083336  
 ; PRIOR FILING DATE: 1998-04-27  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083392  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083495  
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 ; PRIOR APPLICATION NUMBER: 60/083559  
 ; PRIOR FILING DATE: 1998-04-29  
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 ; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: 60/084366  
 ; PRIOR FILING DATE: 1998-05-05  
 ; PRIOR APPLICATION NUMBER: 60/084414  
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 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHGDVSESFVORVYQPLITTCGHRACSTYRTYRATYRSPGL 60  
 DB 20 TEHAYRPGRRVCAVAHGDVSESFVORVYQPLITTCGHRACSTYRTYRATYRSPGL 79  
 QY 61 APARPRVACCPGMRKRTSGLPACGAALICOPPCRNNGSCVQDGRGCRCPAGMRGDTCCQSDVD 120  
 DB 80 APARPRVACCPGMRKRTSGLPACGAALICOPPCRNNGSCVQDGRGCRCPAGMRGDTCCQSDVD 139  
 QY 121 ECSARRGGCPQRCVNTAASYNWCQCEGHSLSADGTLCTPKGGRPRVANNPCVDSAMKEE 180  
 DB 140 ECSARRGGCPQRCVNTAASYNWCQCEGHSLSADGTLCTPKGGRPRVANNPCVDSAMKEE 199  
 QY 181 VORLOSRYVDLLEEXLQVLYAPLHSLASQALEHGLPDPGSLVHSPFOQGRJDSLSEQISF 240  
 DB 200 VORLOSRYVDLLEEXLQVLYAPLHSLASQALEHGLPDPGSLVHSPFOQGRJDSLSEQISF 259  
 QY 241 LEEQUGSCGCKKDS 254  
 DB 260 LEEQUGSCGCKKDS 273

RESULT 5  
 US-09-978-295A-508  
 ; Sequence 508, Application US/09978295A  
 ; Patent No. US20020156006A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
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APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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80 AAPRRYACCPGWRRTSGLPAGCAAIQPPCRNGSSCVQPGRCRCPAGMRGDTCCSDVD 139  
121 ECSARRGGCCPCRCNTVNTGATGSCWCCWEGHSISADGTLGVPGGPPRVAHPNTGVDSANKKE 180  
140 ECSARRGGCCPCRCNTVNTGATGSCWCCWEGHSISADGTLGVPGGPPRVAHPNTGVDSANKKE 199  
181 VQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDPGSLVHSGFQQLGRIDSLSEQISF 240  
200 VQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDPGSLVHSGFQQLGRIDSLSEQISF 259  
241 LEEQLGSCSCCKDS 254

Db 260 LEEQLGSCSCCKDS 273

RESULT 6  
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Sequence 506, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Stewart, Timothy A.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT FILING DATE: 2001-10-16  
CURRENT FILING DATE: 2001-10-16  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;

Best Local Similarity 99.6%; Pred. No. 9.2e-94;

Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ECSARRGGCQPCRVNTAGSYWCQCWEHSLSDAGTLCVPKGGPPRVPANPTGVDSAMKEE 180



Db 140 ECARRGCGCQRCINTGATGWCQWESHSLADGTTLCVPGGPPRAVNPVTGDSANKER 199  
QY 181 VORLOSRVDLLEKRLQVLAPLHSLASQALEHGLPDGSLVHSPQOLGRIDSLSEQISF 240  
Db 200 VORLOSRVDLLEKRLQVLAPLHSLASQALEHGLPDGSLVHSPQOLGRIDSLSEQISF 259  
QY 241 LEEOLGSCSCKKD 254  
Db 260 LEEOLGSCSCKKD 273

RESULT 7  
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Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
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PRIOR FILING DATE: 2001-10-16  
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 140 ECSARRGGCPQRCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPRVAPNPTGVDSAMKEE 199  
QY 181 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLVHVSFQQLGRDLSLSEQISF 240  
DB 200 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLVHVSFQQLGRDLSLSEQISF 259  
QY 241 LBEQLGSCSKKDS 254  
DB 260 LBEQLGSCSKKDS 273  
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US-09-978-192A-506  
; Sequence 506 Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630FIC9  
; CURRENT APPLICATION NUMBER: US/09/978, 192A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641

[illegible]

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| 6  | PRIOR FILING DATE: 1998-04-22        |
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; PRIOR APPLICATION NUMBER: 60/085697

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RESULT 9
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; Sequence 508, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovere, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978.192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-05-13  
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PRIOR APPLICATION NUMBER: 60/085580  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 20 TEHAYRGRVCAVRAHGDVSEFVQRYOPLTTCDGRACSTYRTTAYRSPGL 79  
QY 61 APARPRVACCPGMRKTSGLPGACGAICOPPCRNHGSVOYGRCPAGMRGDTCCSDVD 120  
DB 80 APARPRVACCPGMRKTSGLPGACGAICOPPCRNHGSVOYGRCPAGMRGDTCCSDVD 139  
QY 121 ECSARGGCPQRCVNTAGSYWCQCEHGSLSADGTLCPKGGPRVAPNPTGVDSAMKEE 180  
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RESULT 10  
US-09-790-264-10  
Sequence 10, Application US/09790264  
Patent No. US20020028508A1  
GENERAL INFORMATION:  
APPLICANT: Holzman, Douglas A.  
APPLICANT: Goodheart, Andrew D.J.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
FILE REFERENCE: 0734-322001  
CURRENT APPLICATION NUMBER: US/09/790,264  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
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PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
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PRIOR FILING DATE: 1999-06-22  
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PRIOR FILING DATE: 1998-06-22  
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PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29  
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SEQ ID NO 10  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Homo sapiens

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; LOCATION: (1)...(22)
US-09-790-264-10

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DB 260 LEEQLGSCSKKDS 273

RESULT 11
US-09-790-264-12
; Sequence 12, Application US/09790264
; Patent No. US2002028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Goodenough, Andrew D.J.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-790-264-12

Query Match      98.7%; Score 1392; DB 10; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-92;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPGRRCAVRAHGDVPSEFVQRYVQPFLLTTCGHRACSTYRTIYRTAYRRSPGLAPA 63
DB 1 AYRPGRRCAVRAHGDVPSEFVQRYVQPFLLTTCGHRACSTYRTIYRTAYRRSPGLAPA 60

;
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-790-264-10

Query Match      99.9%; Score 1410; DB 10; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.2e-94;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYVQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 60
DB 20 TEHAYRPGRRCAVRAHGDVPSEFVQRYVQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCSQSDVD 120
DB 80 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCSQSDVD 139

QY 121 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPPRVAPNPTGVDSAMKEE 180
DB 140 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPPRVAPNPTGVDSAMKEE 199

QY 181 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSLSEQISF 240
DB 200 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSLSEQISF 259

QY 241 LEEQLGSCSKKDS 254
DB 260 LEEQLGSCSKKDS 273

RESULT 12
US-09-978-295A-2
; Sequence 2, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/077632
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| 3  | PRIOR APPLICATION NUMBER: 60/078004 |
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| 46 | PRIOR FILING DATE: 1998-04-01       |
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| 56 | PRIOR FILING DATE: 1998-04-09       |
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| 58 | PRIOR FILING DATE: 1998-04-09       |
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| 65 | PRIOR APPLICATION NUMBER: 60/081952 |
| 66 | PRIOR FILING DATE: 1998-04-15       |
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| 69 | PRIOR APPLICATION NUMBER: 60/082568 |
| 70 | PRIOR FILING DATE: 1998-04-21       |
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| 1  | PRIOR FILING DATE: 1998-04-22       |
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| 3  | PRIOR FILING DATE: 1998-04-22       |
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 94.5%; Score 1333; DB 9; Length 295;  
Best Local Similarity 96.8%; Pred. No. 3e-88; Matches 242; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

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DB 106 PRYACCPGKRTSGLPAGCAAIQPPCRNGSCVQPCRCRCPAGMRGDTQSDVDECSA 165  
QY 125 RRGCGPQRCVNTAGSYKQCWEHSLADGTLCPKGGPPVAENPTGVDSAMKEEVQRL 184  
DB 166 RRGCGPQRCVNTAGSYKQCWEHSLADGTLCPKGGPPVAENPTGVDSAMKEEVQRL 225  
QY 185 OSRVDLSEKQLVLAFLHSLASQALEHGLPDPGSLVHSPQQLGRIDSLEQISFLEBQ 244  
DB 226 OSRVDLSEKQLVLAFLHSLASQALEHGLPDPGSLVHSPQQLGRIDSLEQISFLEBQ 285  
QY 245 LGSCSCCKKDS 254  
DB 286 LGSCSCCKKDS 295

RESULT 14  
US-09-978-192A-2  
Sequence 2, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrata, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillman, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT FILING DATE: US/09/978, 192A  
CURRENT FILING DATE: 2001-10-15

1 PRIOR APPLICATION NUMBER: 09/918585  
2 PRIOR FILING DATE: 2001-07-30  
3 PRIOR APPLICATION NUMBER: 60/062250  
4 PRIOR FILING DATE: 1997-10-17  
5 PRIOR APPLICATION NUMBER: 60/064249  
6 PRIOR FILING DATE: 1997-11-03  
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8 PRIOR FILING DATE: 1997-11-13  
9 PRIOR APPLICATION NUMBER: 60/066364  
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11 PRIOR APPLICATION NUMBER: 60/077450  
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25 PRIOR APPLICATION NUMBER: 60/078936  
26 PRIOR FILING DATE: 1998-03-20  
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36 PRIOR FILING DATE: 1998-03-27  
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39 PRIOR APPLICATION NUMBER: 60/079663  
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64 PRIOR FILING DATE: 1998-04-01  
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77 PRIOR APPLICATION NUMBER: 60/081955  
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79 PRIOR APPLICATION NUMBER: 60/081817  
80 PRIOR FILING DATE: 1998-04-15  
81 PRIOR APPLICATION NUMBER: 60/081819  
82 PRIOR FILING DATE: 1998-04-15  
83 PRIOR APPLICATION NUMBER: 60/081952  
84 PRIOR FILING DATE: 1998-04-15  
85 PRIOR APPLICATION NUMBER: 60/081838  
86 PRIOR FILING DATE: 1998-04-15  
87 PRIOR APPLICATION NUMBER: 60/082568  
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89 PRIOR APPLICATION NUMBER: 60/082569  
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91 PRIOR APPLICATION NUMBER: 60/082704  
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100 PRIOR FILING DATE: 1998-04-23  
101 PRIOR APPLICATION NUMBER: 60/083336  
102 PRIOR FILING DATE: 1998-04-27  
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104 PRIOR FILING DATE: 1998-04-28  
105 PRIOR APPLICATION NUMBER: 60/083392  
106 PRIOR FILING DATE: 1998-04-29  
107 PRIOR APPLICATION NUMBER: 60/083495  
108 PRIOR FILING DATE: 1998-04-29  
109 PRIOR APPLICATION NUMBER: 60/083496  
110 PRIOR FILING DATE: 1998-04-29  
111 PRIOR APPLICATION NUMBER: 60/083499  
112 PRIOR FILING DATE: 1998-04-29  
113 PRIOR APPLICATION NUMBER: 60/083545  
114 PRIOR FILING DATE: 1998-04-29  
115 PRIOR APPLICATION NUMBER: 60/083554  
116 PRIOR FILING DATE: 1998-04-29  
117 PRIOR APPLICATION NUMBER: 60/083558  
118 PRIOR FILING DATE: 1998-04-29  
119 PRIOR APPLICATION NUMBER: 60/083559  
120 PRIOR FILING DATE: 1998-04-29  
121 PRIOR APPLICATION NUMBER: 60/083500  
122 PRIOR FILING DATE: 1998-04-29  
123 PRIOR APPLICATION NUMBER: 60/083742  
124 PRIOR FILING DATE: 1998-04-30  
125 PRIOR APPLICATION NUMBER: 60/084366  
126 PRIOR FILING DATE: 1998-05-05  
127 PRIOR APPLICATION NUMBER: 60/084414  
128 PRIOR FILING DATE: 1998-05-06  
129 PRIOR APPLICATION NUMBER: 60/084441  
130 PRIOR FILING DATE: 1998-05-06  
131 PRIOR APPLICATION NUMBER: 60/084637  
132 PRIOR FILING DATE: 1998-05-07  
133 PRIOR APPLICATION NUMBER: 60/084639  
134 PRIOR FILING DATE: 1998-05-07  
135 PRIOR APPLICATION NUMBER: 60/084640  
136 PRIOR FILING DATE: 1998-05-07  
137 PRIOR APPLICATION NUMBER: 60/084598  
138 PRIOR FILING DATE: 1998-05-07  
139 PRIOR APPLICATION NUMBER: 60/084600  
140 PRIOR FILING DATE: 1998-05-07  
141 PRIOR APPLICATION NUMBER: 60/084627  
142 PRIOR FILING DATE: 1998-05-07  
143 PRIOR APPLICATION NUMBER: 60/084643  
144 PRIOR FILING DATE: 1998-05-07  
145 PRIOR APPLICATION NUMBER: 60/085339  
146 PRIOR FILING DATE: 1998-05-13

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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          94.5%; Score 133; DB 9; Length 295;
Best Local Similarity 96.8%; Pred. No. 3e-88;
Matches 242; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```

```

QY 7 PGRRCAY--RAHGDVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGLAPAR 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46 PARPGCVLSTAHGDPVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGLAPAR 105
QY 65 PRVACCPGKRTSGLPAGCGAATCOPPCRNAGSCVQPGRCRCPAGWRGDTGQSDVDCSA 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 106 PRVACCPGKRTSGLPAGCGAATCOPPCRNAGSCVQPGRCRCPAGWRGDTGQSDVDCSA 165
QY 125 RRGCPQRCVNTAGSYWCQWEGHSLSDGTLVCPKGGPRVAPNPVGVDSAMKEVQRL 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 RRGCPQRCVNTAGSYWCQWEGHSLSDGTLVCPKGGPRVAPNPVGVDSAMKEVQRL 225
QY 185 QSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLVHVSQQLGRIDSLSEQISFLEEQ 244
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226 QSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLVHVSQQLGRIDSLSEQISFLEEQ 285
QY 245 LGSCSCCKDS 254
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286 LGSCSCCKDS 295

```

```

RESULT 15
US-09-790-264-15
; Sequence 15, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: US95
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29

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; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-15

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Query Match          80.8%; Score 1139.5; DB 10; Length 275;
Best Local Similarity 79.9%; Pred. No. 1.6e-74;
Matches 203; Conservative 16; Mismatches 34; Indels 1; Gaps 1;

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```

QY 1 TEHAYRPGRRVCAVRAHGDVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 TEHAYRPSRRVCTVIGSGSISLTFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGL 80
QY 61 APPRPRIACCPGKRTSGLPAGCGAATCOPPCRNAGSCVQPGRCRCPAGWRGDTGQSDVD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 TPAPRPRIACCPGKRTSGLPAGCGAATCOPPCRNAGSCVQPGRCRCPAGWRGDTGQSDVD 140
QY 121 ECGARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLVCPKGGPRVAPNPVGVDSAMKE 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 ECGTGAASCPQRCVNTAGSYWCQWEGHSLSDGTLVCPKGGPRVAPNPVGVDSAMKE 200
QY 180 EYQRLQSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLVHVSQQLGRIDSLSEQIS 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 EYVRLQARVDVLEKQLVLAFLHSLASQALEHGLPDPGSLVHVSQQLGRIDSLSEQIS 260
QY 240 FLEHLLGSCSCCKD 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 261 FLEHLLGSCSCCKD 274

```

```

Search completed: December 17, 2002, 10:09:46
Job time : 9.1955 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:00:11 ; Search time 13.9772 Seconds  
(without alignments)  
1746.994 Million cell updates/sec

Title: US-09-852-472-3

Perfect score: 1411  
Sequence: 1 THNAVPRGRVCAVARHGP.....SEQISFLEQLGSCSCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description          |
|------------|-------|-------------|--------|----------|----------------------|
| 1          | 425   | 30.1        | 293    | 2 T09065 | hypothetical prote   |
| 2          | 257   | 18.2        | 1574   | 2 T13954 | MEG6 protein - ra    |
| 3          | 253.5 | 18.0        | 558    | 2 T17324 | hypothetical prote   |
| 4          | 219   | 15.5        | 1620   | 2 T27283 | hypothetical prote   |
| 5          | 196   | 13.9        | 1964   | 2 T09059 | notch4 - mouse       |
| 6          | 189   | 13.4        | 678    | 2 B48089 | growth arrest-spec   |
| 7          | 184   | 13.0        | 673    | 2 A48089 | growth arrest-spec   |
| 8          | 181   | 12.8        | 810    | 2 T10756 | Nel-homolog protein  |
| 9          | 178   | 12.6        | 674    | 2 T55476 | growth potentialin   |
| 10         | 175.5 | 12.4        | 3002   | 2 A47221 | fibritillin 1 precu  |
| 11         | 175   | 12.4        | 2907   | 2 A57278 | fibritillin-2 precu  |
| 12         | 174.5 | 12.3        | 2321   | 2 S78549 | notch3 protein - h   |
| 13         | 173.5 | 12.3        | 1247   | 1 M4HUND | notch3 protein - h   |
| 14         | 173   | 12.3        | 835    | 2 JPO076 | nidogen precursor    |
| 15         | 172   | 12.2        | 2531   | 2 A46019 | Notch-1 protein -    |
| 16         | 171.5 | 12.2        | 2871   | 2 A55624 | fibritillin-1 precu  |
| 17         | 170.5 | 12.1        | 2871   | 2 A55624 | fibritillin-1 - bovi |
| 18         | 170   | 12.0        | 675    | 1 KXMS   | plasma protein S p   |
| 19         | 169   | 12.0        | 2703   | 1 A24420 | notch protein - fr   |
| 20         | 168.5 | 11.9        | 2318   | 2 S45306 | notch 3 protein -    |
| 21         | 168   | 11.9        | 675    | 1 KXMS   | plasma protein S p   |
| 22         | 168   | 11.9        | 833    | 2 S19087 | gene Delta protein   |
| 23         | 165   | 11.7        | 832    | 2 A31246 | neurogenic protei    |
| 24         | 165   | 11.7        | 880    | 2 S00670 | neurogenic repetit   |
| 25         | 165   | 11.7        | 2524   | 2 A35844 | Xotch protein - Af   |
| 26         | 164.5 | 11.7        | 2918   | 2 A54105 | fibritillin-2 precu  |
| 27         | 164   | 11.6        | 1429   | 2 S06434 | homeotic protein 1   |
| 28         | 164   | 11.6        | 2555   | 2 A40043 | notch protein homo   |
| 29         | 163   | 11.6        | 3871   | 2 T22812 | hypothetical prote   |

|    |       |      |      |          |                     |
|----|-------|------|------|----------|---------------------|
| 30 | 162   | 11.5 | 387  | 2 B49175 | Notch A protein -   |
| 31 | 162   | 11.5 | 646  | 2 S38819 | plasma protein S -  |
| 32 | 162   | 11.5 | 675  | 1 KXBO   | plasma protein S p  |
| 33 | 160.5 | 11.4 | 2531 | 2 S18188 | notch protein homo  |
| 34 | 160   | 11.3 | 2437 | 2 S42612 | transmembrane prot  |
| 35 | 159.5 | 11.3 | 407  | 1 KFB07  | coagulation factor  |
| 36 | 159   | 11.2 | 1820 | 2 A55494 | latent transformin  |
| 37 | 158.5 | 11.2 | 456  | 1 KXBO   | protein C (activat  |
| 38 | 157   | 11.1 | 676  | 1 KKHUS  | plasma protein S p  |
| 39 | 157   | 11.1 | 1221 | 2 A49457 | fibritillin-2 precu |
| 40 | 156   | 11.1 | 642  | 2 S53434 | plasma protein S p  |
| 41 | 155   | 11.0 | 387  | 2 T38449 | extracellular prote |
| 42 | 155   | 11.0 | 1408 | 2 S16148 | gene serrate prote  |
| 43 | 154   | 10.9 | 642  | 2 S53433 | plasma protein S p  |
| 44 | 154   | 10.9 | 1220 | 2 A56136 | jagged protein pre  |
| 45 | 153.5 | 10.9 | 861  | 2 A48825 | Notch homolog Motc  |

## ALIGNMENTS

## RESULT 1

T09065

hypothetical protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jan-2000

C:Accession: T09065

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sci

submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543

A:Accession: T09065

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-293 <ROM>

A:Cross-references: EMBL:AF030001; NID:G2564945; PID:G2564953

C:Genetics:

A:Map position: 17

C:Superfamily: unassigned EGF-related proteins; EGF homology

F:114-141/Domain: EGF homology <EGF1>

F:148-183/Domain: EGF homology <EGF>

Query Match 30.1%, Score 425; DB 2; Length 293;

Best Local Similarity 37.3%, Pred. No. 4,7e-24;

Matches 103; Conservative 34; Mismatches 95; Indels 44; Gaps 11;

|    |     |   |  |
|----|-----|---|--|
| QY | 4   | AYRPRRVCAVARHGPV--SESFVQRYVQPFITTCGHRACSTYRTTYRAYSPELA 61     |  |
| DB | 30  | SPKESLGVCSKOTLLVPRVNESYSQPYKPYTLTCAGRRICSTYRTTYRVAMREVRREV 89 |  |
| QY | 62  | PAPRYACCPGCKRTSGA--GAAGA--AICQPCRMGSGCVQGRCPAGMGDPCCQSDVD 120 |  |
| DB | 90  | P-QTHVCCQCKKPH--FGALTCDAICSKPCLVGGVCTGPDCECAPGMCKCHVDVD 146   |  |
| QY | 121 | ECSSARRGCPQRCVNTAGSYWCQCEGHSLSADGTLCPKSGPRVAVNPPTGV----- 173  |  |
| DB | 147 | ECRAFLTICSHGCLNTLGSFLSCPHPLVLDGRICA--GGPE---SPISAILSVAV 201   |  |
| QY | 174 | -----DSMKKEYQLQSRVDLLEKQLVLAPLHLSAQA---LEHGIP-DPGSLIV 222     |  |
| DB | 202 | READEERARLRMEVAEIRGRLEKLEQ-----WATQAGAWRAVAVPMPPEIRP 250      |  |
| QY | 223 | HSFOQL-----GRISLSQISFLEQLGSCSCKKDS 254                        |  |
| DB | 251 | EOVAELMGKGRDRIISLSDVLLERLGAACACEDNS 286                       |  |

## RESULT 2

T13954

MEG6 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T13954  
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
 Genomics 51, 27-34, 1998  
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
 A:Reference number: 214126; MUID:98360089; PMID:9693030  
 A:Accession: T13954  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1574 <NAK>  
 A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294  
 A:Experimental source: strain Sprague-Dawley; brain  
 C:Genetics:  
 A:Gene: MEGF6

Query Match 18.2%; Score 257; DB 2; Length 1574;  
 Best Local Similarity 38.5%; Pred. No. 4.1e-11;  
 Matches 65; Conservative 15; Mismatches 61; Indels 28; Gaps 9;  
 QY 11 VCAVR-----AHGDPVSEFVQRYVQPLTTCDGHRAC--STYETIYRTAYRRSPGLAPA 63  
 DB 43 VCAEQKFLVGHQPCVQAFSRIVPVWRRTGCAQQAACIGQERRIVYMSYRQVYA-TEA 101  
 QY 64 RPRVACCPGKRTSLPGA-----CGAAI--CQPPCRN--GGSCVQPGRCRCPAGWR-- 111  
 DB 102 RTVFRCCFGMSQKPGQEGCLSDVDECASANGCGPCNTVGGF-----YRCPPGYQLQ 156  
 QY 112 --GDTCSQSDVDECSARRGCGPQRCVNTAGSYWCQCGHLSADGTLGV 158  
 DB 157 GDGKTCQ-DVDECAHGGCGHRCVNTPGSYLCECKPFLHTDGTCL 204

RESULT 3  
 T17324  
 hypothetical protein DKFp564P2063.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17324  
 R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18727  
 A:Accession: T17324  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-558 <DUE>  
 A:Cross-references: EMBL:AL117610  
 A:Experimental source: fetal brain; clone DKFp564P2063  
 C:Genetics:  
 A:Note: DKFp564P2063.1

Query Match 18.0%; Score 253.5; DB 2; Length 558;  
 Best Local Similarity 37.4%; Pred. No. 3e-11;  
 Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;  
 QY 39 GHRACSTVTTIYRTAYRRSPGLAPAPRYACCPGKRTSLPGACGAAICQPPCRNGGSC 98  
 DB 26 GNAASARHHGLASA--RQPGVCHYGTKLACCYWRNRS--KGV-C-PAETCEPGCK-FGEC 79  
 QY 99 VQPGRCRCPAGWRGDTCSQSDVDECSARRGCGPQRCVNTAGSYWCQCGHLSADGTLGV 158  
 DB 80 VGPNNKRCCLPGVGTGKTSQDVNECGMKPRPCQHRKCVNTHSGYKFCFLSGHMLMDAT-CV 138  
 QY 159 -----PKGGPP-----RVAEN 169  
 DB 139 YSRTCAMINQVSCEDTBEGPQLCPSSGLRLAPN 173

RESULT 4  
 T27283  
 hypothetical protein y64G10A.f - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T27283  
 R:Ainscough, R.

submitted to the EMBL Data Library, September 1999  
 A:Reference number: Z20336  
 A:Accession: T27283  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1620 <WIL>  
 A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CBSP:Y64G10A.f  
 A:Experimental source: clone Y64G10A  
 C:Genetics:  
 A:Gene: CBSP:Y64G10A.f  
 A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;

Query Match 15.5%; Score 219; DB 2; Length 1620;  
 Best Local Similarity 41.3%; Pred. No. 2.6e-08;  
 Matches 43; Conservative 8; Mismatches 35; Indels 18; Gaps 4;  
 QY 83 CGAAICQPPCRNGGSCVQPGR-----CRCPAGWRGDTCSQSDVDECSARRGCGPQRCVNT 136  
 DB 79 CSADL-----CHNGGTCTVPSEHNDNEQVCECPVGTGAKCOYDANECAWNGGCEHCYNT 134  
 QY 137 ASGYWCQCGHLSADGTLG-----VPKGG-PPRVAPNPTG 172  
 DB 135 IGTYTCRCWPGFELSGDGNCTSDIDECAVSNCGSCDRCVNSPG 178

RESULT 5  
 T09059  
 notch4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-2000  
 C:Accession: T09059  
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;  
 submitted to the EMBL Data Library, October 1997  
 A:Description: Sequence of the mouse major histocompatibility locus class III region.  
 A:Reference number: Z16543  
 A:Accession: T09059  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1964 <ROW>  
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947  
 C:Genetics:  
 A:Gene: notch4  
 A:Map position: 17  
 A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1;  
 1679/3; 1729/1; 1761/3  
 C:Superfamily: unassigned EGF-related proteins; EGF homology  
 C:Keywords: receptor; signal transduction  
 F:514-545/Domain: EGF homology <EGF>

Query Match 13.9%; Score 196; DB 2; Length 1964;  
 Best Local Similarity 34.2%; Pred. No. 1.5e-06;  
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;  
 QY 61 APARPRYACCPGK-RTSGLPAGCAATCQPPCRNGGSCVQPG---RCRCPAGWRGDTQ 116  
 DB 134 ASGRQCSCSEPWTEGQQLRDFCSA----NPCANGVCLATYPOICRCPPGEGHTCE 189  
 QY 117 SDVDECSARRGCGPQ--RCVNTAGSYWCQ---WEGHLSADGTLGV---KGGPPRVA 167  
 DB 190 RDINECFLEPGPCPQOTSCHNTLSYQCLCPVQGGPQCKLRKGACPPGSCINGGTCLV 249  
 QY 168 PNP-----TGVDSSMKEE 180  
 DB 250 PEGHSTFHLCLCPPGFTGLDCENMPD 275

RESULT 6  
 B48089  
 growth arrest-specific protein gas6 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999  
 C:Accession: B48089  
 R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.

Mol. Cell. Biol. 13, 4976-4985, 1993  
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: B48089

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-678 <MAN>

C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom

F:120-153/Domain: EGF homology <EG1>

F:160-195/Domain: EGF homology <EG2>

F:201-236/Domain: EGF homology <EG3>

F:242-277/Domain: EGF homology <EG4>

F:311-671/Domain: sex hormone-binding globulin homology <SHB>

F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 13.4%; Score 189; DB 2; Length 678;

Best Local Similarity 34.2%; Pred. No. 1.9e-06;

Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Db 27 QRYVQPELTCDG-----RACSTYRTYRTAYRRSPGLAPAPRYACC-----PGMK 74

Db 47 RRARQVEBAKQGLERECVEBELCS--REARREVFENDPETYFYPYIDCINKKGYSPYT 104

Qy 75 RTSG-----LPGACGAAICOPPC--RNGSCVQP--GR--CRCPAGMRGDTQSDVDEC 122

Db 105 KNSGFATCVQNLDPQC-----TPNPCRKGTQACDLMGNFCLCKKAGMGRLCDKXVNEC 160

Qy 123 SARRGCPQRCVNTAGSYWCQCEGSHSLADGTLG 157

Db 161 SQENGGLQICHNKPGSGFHCSCSGFELSSDGRIC 195

RESULT 7

A48089

growth arrest-specific protein gas6 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999

C:Accession: A48089; S37437

R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.

Mol. Cell. Biol. 13, 4976-4985, 1993

A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: A48089

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-673 <MAN>

A:Cross-references: GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061

A:Note: authors translated the codon CCC for residue 424 as Ile

C:Gene: gas6

C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom

F:38-89/Domain: EGF homology <EG1>

F:117-150/Domain: EGF homology <EG2>

F:157-192/Domain: EGF homology <EG3>

F:198-233/Domain: EGF homology <EG4>

F:239-274/Domain: EGF homology <EG5>

F:308-666/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 13.0%; Score 184; DB 2; Length 673;

Best Local Similarity 31.6%; Pred. No. 4.3e-06;

Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

Qy 27 QRYVQPELTCDG-----RACSTYRTYRTAYRRSPGLAPAPRYACC-----70

Db 44 RRARQVEBAKQGLERECVEBELCS--REARREVFENDPETYFYPYIDCINKKGYSPYT 101

Qy 71 --PGMK--TSGLPAC-----GAALCOPPCNNGSCVQPGRCRCPCAGMRGDTQSDV 119

Db 102 KNPDFAKVQNLDPQCETPNPCDKKGTTHICODLMGN-----FFCVCTDGMGRGLCDKV 154

Qy 120 DECSARRGGCPQRCVNTAGSYWCQCEGSHSLADGTLG 157

Db 155 NECVQKNGGCGSQVCHNKPGSRQACGSGFSLASDQTC 192

RESULT 8

T10756

Nel-homolog protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C:Accession: T10756

R:Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsubashi, S.; Kikkawa, U.

submitted to the EMBL Data Library, November 1998

A:Description: Protein kinase C-binding protein.

A:Reference number: 217122

A:Accession: T10756

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-810 <KTR>

A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180

A:Experimental source: strain Sprague-Dawley, brain

Query Match 12.8%; Score 181; DB 2; Length 810;

Best Local Similarity 37.5%; Pred. No. 8.4e-06;

Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

Qy 69 CCRPKRRTSGLPAGAGALICOPPCNNGSCVQPGRCRCPCAGMRGDTQSDVDECSARRG 128

Db 504 CQPGVGN-----GTICKAFCEGGRYGTGVAIPKVCPSGFTSGHCKEIDCEAGFVE 559

Qy 129 CP--ORCVNTAGSYWCQCEGH---SLADGTLGV 158

Db 560 CHNYSRCVNLPGMHYHCBRSRSPHDDGTSLSGESCI 595

RESULT 9

155476

growth potentiating factor - rat

C:Species: Rattus sp. (rat)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001

C:Accession: 155476

R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.

J. Biol. Chem. 270, 5702-5705, 1995

A:Title: Vascular smooth muscle cell-derived, Glu-containing growth-potentiating factor

A:Reference number: 155476; MUID:95197586; PMID:7890695

A:Accession: 155476

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-674 <RBS>

A:Cross-references: GB:D42148; NID:91526567; PIDN:BA07719.1; PID:9893402

C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom

F:29-89/Domain: EGF homology <EG1>

F:117-150/Domain: EGF homology <EG2>

F:157-192/Domain: EGF homology <EG3>

F:198-233/Domain: EGF homology <EG4>

F:239-274/Domain: EGF homology <EG5>

F:308-667/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 12.6%; Score 178; DB 2; Length 674;

Best Local Similarity 30.4%; Pred. No. 1.2e-05;

Matches 48; Conservative 8; Mismatches 66; Indels 36; Gaps 6;

Qy 27 QRYVQPELTCDG-----RACSTYRTYRTAYRRSPGLAPAPRYACC-----70

Db 44 RRARQVEBAKQGLERECVEBELCS--REARREVFENDPETYFYPYIDCINKKGYSPYT 101

Qy 71 --PGMK--TSGLPAC-----GAALCOPPCNNGSCVQPGRCRCPCAGMRGDTQSDV 119

Db 102 KNPDFAKVQNLDPQCETPNPCDKKGTQCDLMGN-----FFCLCKDGMGRGLCDKV 154

C;Species: Homo sapiens (man)

7-1-



C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Aug-2002  
 C/Accession: S78549; S71825  
 R/Jourel, A.; Tourmlier-Lasserve, E.  
 Submitted to the EMBL Data Library, April 1997  
 A/Reference number: S78549  
 A/Accession: S78549  
 A/Molecule type: mRNA  
 A/Residues: 1-2321 <JOU1>  
 A/Cross-references: EMBL:U97669; NID:g2668591; PID:ABE91371.1; PID:g2668592  
 R/Jourel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowicz  
 X, M.M.; Weissbach, J.; Bach, J.F.; Bousser, M.G.; Tourmlier-Lasserve, E.  
 Nature 383, 707-710, 1996  
 A/Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke  
 A/Reference number: S71825; MUID:97032728; PMID:8878478  
 A/Accession: S71825  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 67-113,138-194,268-333, 'G', 335-346,536-613,716-765,1240-1279,1815-1888 <JOU2  
 A/Cross-references: EMBL:U97669  
 C/Genetics:  
 A:Gene: notch3  
 A:Map position: 19p13.1  
 C/Function:  
 A/Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and  
 C/Superfamily: notch protein; ankyrin repeat homology; EGF homology; laminin-type EGF-1  
 C/Keywords: tandem repeat; transmembrane protein  
 F:123-155/Domain: EGF homology <EGF1>  
 F:162-194/Domain: EGF homology <EGF1>  
 F:240-271/Domain: EGF homology <EGF1>  
 F:318-349/Domain: EGF homology <EGF>  
 F:473-504/Domain: EGF homology <EGF>  
 F:853-884/Domain: EGF homology <EGF3>  
 F:928-959/Domain: EGF homology <EGF4>  
 F:1070-1126/Domain: laminin-type EGF-like homology <LEG>  
 F:1838-1870/Domain: ankyrin repeat homology <AN1>  
 F:1871-1903/Domain: ankyrin repeat homology <AN2>  
 F:1905-1937/Domain: ankyrin repeat homology <AN3>  
 F:1938-1970/Domain: ankyrin repeat homology <AN4>  
 F:1971-2003/Domain: ankyrin repeat homology <AN5>  
 Query Match 12.4%; Score 174.5; DB 2; Length 2321;  
 Best local similarity 34.5%; Pred. No. 6,4e-05;  
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;  
 QY 37 CDGHACSTYRTYRTAVRSPGLAPRPYAC-CPEMKR--ISGLPGAGAIICPPCR 93  
 Db 87 CAGKRVCS-----SVAGTARPSCKPCRGFGPDCSLPDC---LSSPCA 129  
 QY 94 NGGSC-VDP-GR--CRCPAGWRGDTCCSDVDCE---SARRGGCPRCVNTAGSYWCCGM 145  
 Db 130 HGACSVGPDGRFLCSGPGYQGRSCLSDVDCEVGRPCHHG---TCLNTPGSRFCQCP 186  
 QY 146 EGHSLSDAGTLCVKGKGPVAVNP 170  
 Db 187 AGYT---GPLCENPAVP--CAPSP 205  
 RESULT 13  
 MGHUND  
 nidogen precursor - human  
 N/Alternate names: entactin  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Oct-2000  
 C/Accession: A33322; A32437; A61367  
 R/Nagayoshi, T.; Sabhorn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlton  
 DNA 8, 581-594, 1989  
 A/Title: Human nidogen: complete amino acid sequence and structural domains deduced from  
 A/Accession: A33322; MUID:90091745; PMID:2574658  
 A/Reference number: A33322  
 A/Molecule type: mRNA  
 A/Residues: 1-1247 <NAG>  
 A/Cross-references: EMBL:M30269  
 R/Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.;

Am. J. Hum. Genet. 44, 876-885, 1989  
 A/Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to chr  
 A/Reference number: A32437; MUID:89270475; PMID:2471408  
 A/Accession: A32437  
 A/Molecule type: mRNA  
 A/Residues: 667-1247 <OLS>  
 A/Cross-references: EMBL:M27445; NID:g602466; PID:AAA57261.1; PID:g602467  
 A/Note: the authors translated the codon AAG for residue 966 as Cys  
 J. Invest. Dermatol. 97, 281-285, 1991  
 A/Title: Human nidogen gene: structural and functional characterization of the 5'-flankir  
 A/Reference number: A61367; MUID:91302882; PMID:1906509  
 A/Accession: A61367  
 A/Molecule type: DNA  
 A/Residues: 1-28 <FAZ>  
 C/Comment: This protein is a basement membrane glycoprotein that forms a complex with lan  
 C/Genetics:  
 A:Gene: GDB:NID  
 A/Cross-references: GDB:120236; OMIM:131390  
 A:Map position: 1q43-1q43  
 C/Superfamily: nidogen; EGF homology; LDL receptor WYTD-containing repeat homology; thyr  
 C/Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; cel  
 protein  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-1247/Product: nidogen #status predicted <WAT>  
 F:390-425/Domain: EGF homology <EG1>  
 F:672-708/Domain: EGF homology <EG2>  
 F:702-704/Region: cell attachment (R-G-D) motif  
 F:714-750/Domain: EGF homology <EG3>  
 F:762-800/Domain: EGF homology <EG4>  
 F:806-839/Domain: EGF homology <EG5>  
 F:890-919/Domain: thyroglobulin type I repeat homology <THY1>  
 F:990-1032/Domain: LDL receptor WYTD-containing repeat homology <WY1>  
 F:1033-1075/Domain: LDL receptor WYTD-containing repeat homology <WY2>  
 F:1076-1120/Domain: LDL receptor WYTD-containing repeat homology <WY3>  
 F:1121-1160/Domain: LDL receptor WYTD-containing repeat homology <WY4>  
 F:1161-1197/Domain: LDL receptor WYTD-containing repeat homology <WY5>  
 F:1212-1243/Domain: LDL receptor WYTD-containing repeat homology <WY6>  
 F:1289,296/Binding site: sulfate (Tyr) (covalent) #status predicted  
 F:729,819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F:756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #status predict  
 F:1137/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 12.3%; Score 173.5; DB 1; Length 1247;  
 Best local similarity 25.8%; Pred. No. 4,4e-05;  
 Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;  
 QY 1 TEHAYRRGRV-----CAVAAH-----DPVSESFVQRYVQPLTTCDGHACSTYR 47  
 Db 681 TNACRGRGPTPTCECSIGFRDGRTCYDIDECSE-----QP--SYCGSHTCNNH- 730  
 QY 48 TIYTAVRSPGLAPRPYACCPGKRTSGLPAGCAIICPP--CRNG----- 95  
 Db 731 -----PGRFCEVGEYQPSD--EGTCVAVDPRPNTYCEGTGLHNCIDPQR 774  
 QY 96 GSCVQPG---RCRCPAGWRGD--TCQSDVDECSARRGGCPQRCVNTAGSYWCCWEGHS 149  
 Db 775 AQCITYGSSSYTSCLPGRSGDQACQ--DVDECQSRCHPDAFCVNTGSGFTCCQCKPGY- 832  
 QY 150 LSAAGTLCVP-----KGPPVAVNPFG----- 172  
 Db 833 -QGDGRFVGEVEKTRCQHEEHILGAAGATDPQRPPIPGILFVECDAGHYAPTCQHG 891  
 QY 173 -----VDSAMEEYQRLQSRVDLLEKLCQVLAFLH--SLASQALEHGLDPPSLVHS 224  
 Db 892 STGYCWCVDPRDG--EVEGRTTRPGMTTPCLSTVAPPIHQGPAVPAVPLP--PGTHLL-- 947  
 QY 225 FQQLGRIDSL 234  
 Db 948 FAQTGKIERTL 957  
 RESULT 14

JP00076  
 nel protein - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 13-Aug-1999  
 C:Accession: A38963; JP00076  
 R:Matsumoto, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.  
 Dev. Dyn. 203, 212-222, 1995  
 A:Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressed in the developing chicken embryo  
 A:Reference number: A38963; MUID:95383734; PMID:7655083  
 A:Accession: A38963  
 A:Molecule type: mRNA  
 A:Residues: 1-835 <MAT>  
 A:Cross-references: DDBJ:D45365  
 A:Experimental source: 9-day embryo  
 R:Matsumoto, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.  
 submitted to JIPID, January 1995  
 A:Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressed in the developing chicken embryo  
 A:Reference number: JP00076  
 A:Accession: JP00076  
 A:Molecule type: mRNA  
 A:Residues: 1-835 <MA2>  
 A:Cross-references: DDBJ:D45365  
 A:Experimental source: 9-day embryo  
 C:Superfamily: von Willebrand factor type C repeat homology; EGF homology  
 F:273-333/Domain: von Willebrand factor type C repeat homology <VMC>  
 F:395-592/Region: EGF-like repeats  
 F:444-480/Region: EGF homology <EGF1>  
 F:486-521/Domain: EGF homology <EGF>  
 F:525-552/Domain: EGF homology <EGF2>

Query Match 12.3%; Score 173; DB 2; Length 835;  
 Best Local Similarity 41.4%; Pred. No. 3.3e-05;  
 Matches 29; Conservative 12; Mismatches 27; Indels 2; Gaps 1;  
 QY 81 GACGAAICPPNNGSCVQPCRCPCAGWRCGTCSQDVDECSARRGGCPOR--CVNTAG 138  
 DB 518 GTVCKAFCKDGRNGACTASNVACPCQPGFTGSCETDIDECSDGDFVQDSRANCINLP 577  
 QY 139 SYWCQCEGH 148  
 DB 578 WYHCECRDGY 587

RESULT 15  
 A46019  
 Notch-1 protein - mouse  
 N:Alternate names: notch protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Sep-1999  
 C:Accession: A46019; S25144  
 R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid  
 Genomics 15, 259-264, 1993  
 A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of  
 A:Reference number: A46019; MUID:93194170; PMID:8449489  
 A:Accession: A46019  
 A:Status: not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-2531 <DEL>  
 A:Cross-references: GB:S47228; NID:g288502; PIDN:CAA77941.1; PID:g288503  
 A:Note: sequence extracted from NCBI backbone (NCBIP:127318)  
 R:Francisco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests  
 A:Reference number: S25144  
 A:Accession: S25144  
 A:Molecule type: mRNA  
 A:Residues: 1551-2108, Q', 2110-2114, 'ALP', 2118-2170 <FRA>  
 A:Cross-references: EMBL:Z11886  
 C:Genetics:  
 A:Gene: notch-1  
 A:Map position: 2  
 A:Note: proximal region of chromosome 2  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

F:106-138/Domain: EGF homology <EGF1>  
 F:144-175/Domain: EGF homology <EGF1>  
 F:222-254/Domain: EGF homology <EGF2>  
 F:261-292/Domain: EGF homology <EGF2>  
 F:339-370/Domain: EGF homology <EGF3>  
 F:416-449/Domain: EGF homology <EGF3>  
 F:456-487/Domain: EGF homology <EGF4>  
 F:494-525/Domain: EGF homology <EGF5>  
 F:532-563/Domain: EGF homology <EGF6>  
 F:607-638/Domain: EGF homology <EGF7>  
 F:682-713/Domain: EGF homology <EGF8>  
 F:757-788/Domain: EGF homology <EGF9>  
 F:795-826/Domain: EGF homology <EGF10>  
 F:873-904/Domain: EGF homology <EGF11>  
 F:911-942/Domain: EGF homology <EGF12>  
 F:949-980/Domain: EGF homology <EGF13>  
 F:987-1018/Domain: EGF homology <EGF14>  
 F:1025-1056/Domain: EGF homology <EGF15>  
 F:1063-1094/Domain: EGF homology <EGF16>  
 F:1149-1180/Domain: EGF homology <EGF17>  
 F:1187-1218/Domain: EGF homology <EGF18>  
 F:1233-1264/Domain: EGF homology <EGF19>  
 F:1352-1383/Domain: EGF homology <EGF20>  
 F:1391-1425/Domain: EGF homology <EGF21>  
 F:1493-1581/Domain: ankyrin repeat homology <AN1>  
 F:1583-2015/Domain: ankyrin repeat homology <AN2>  
 F:2016-2048/Domain: ankyrin repeat homology <AN3>  
 F:2049-2081/Domain: ankyrin repeat homology <AN4>  
 F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 12.2%; Score 172; DB 2; Length 2531;  
 Best Local Similarity 34.5%; Pred. No. 0.0001;  
 Matches 41; Conservative 5; Mismatches 37; Indels 36; Gaps 5;  
 QY 69 CCGWKRTSGLPGACGAATCQP-----PCRNNGSCV---QPCRCPCAGWRCGTCSQD 118  
 DB 129 CSFGWSGKS-----CQADPCASNPANGGQCLPFESSYICRCPPGPHGPTCRD 178  
 QY 119 VDECSARRGGCPQ--PCVNTAGSYWCQCEGH-----SLSDGTLCVPGK 161  
 DB 179 VNECSQNPGLCRHGHCHNEIGSYRCACCATHTGPHCELPYVPCSPSPQNGATCRPTG 237

Search completed: December 17, 2002, 10:03:40  
 Job time : 16.9772 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 09:45:16 ; Search time 8.19355 Seconds  
(without alignments)  
1285.766 Million cell updates/sec

Title: US-09-852-472-3  
Perfect score: 1411  
Sequence: 1 TEHAYRPGRRVCVRAHGP.....SEQISFLERQLGSCCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 196   | 13.9        | 1964   | 1     | NTC4_MOUSE  |
| 2          | 188.5 | 13.4        | 2003   | 1     | NTC4_HUMAN  |
| 3          | 184   | 13.0        | 816    | 1     | NEL2_MOUSE  |
| 4          | 183   | 13.0        | 810    | 1     | NEL1_HUMAN  |
| 5          | 181.5 | 12.9        | 816    | 1     | NEL2_HUMAN  |
| 6          | 181   | 12.8        | 810    | 1     | NEL1_RAT    |
| 7          | 179.5 | 12.7        | 816    | 1     | NEL2_RAT    |
| 8          | 176   | 12.5        | 652    | 1     | CD93_HUMAN  |
| 9          | 175.5 | 12.4        | 816    | 1     | NEL_CHICK   |
| 10         | 175.5 | 12.4        | 2871   | 1     | FBN1_HUMAN  |
| 11         | 175   | 12.4        | 2907   | 1     | FBN2_MOUSE  |
| 12         | 174.5 | 12.4        | 2321   | 1     | NTC3_HUMAN  |
| 13         | 173.5 | 12.3        | 1247   | 1     | NIDO_HUMAN  |
| 14         | 172   | 12.2        | 2531   | 1     | NTC1_MOUSE  |
| 15         | 171.5 | 12.2        | 2871   | 1     | FBN1_MOUSE  |
| 16         | 171   | 12.1        | 2703   | 1     | NOTC_MOUSE  |
| 17         | 170.5 | 12.1        | 2871   | 1     | NOTC_DROME  |
| 18         | 170   | 12.0        | 675    | 1     | FBN1_BOVIN  |
| 19         | 169.5 | 12.0        | 2871   | 1     | PRTS_MOUSE  |
| 20         | 168.5 | 11.9        | 2318   | 1     | NTC3_MOUSE  |
| 21         | 168   | 11.9        | 675    | 1     | PRTS_RAT    |
| 22         | 168   | 11.9        | 833    | 1     | DL_DROME    |
| 23         | 166   | 11.8        | 1238   | 1     | JAG2_HUMAN  |
| 24         | 166   | 11.8        | 1247   | 1     | JAG2_MOUSE  |
| 25         | 165   | 11.7        | 1202   | 1     | JAG2_RAT    |
| 26         | 165   | 11.7        | 2524   | 1     | NOTC_XENTLA |
| 27         | 164.5 | 11.7        | 2911   | 1     | FBN2_HUMAN  |
| 28         | 164   | 11.6        | 1429   | 1     | LIT2_CAEL   |
| 29         | 163   | 11.6        | 2556   | 1     | NTC1_HUMAN  |
| 30         | 162   | 11.5        | 644    | 1     | CD93_MOUSE  |
| 31         | 162   | 11.5        | 646    | 1     | PRTS_RABIT  |
| 32         | 162   | 11.5        | 675    | 1     | PRTS_BOVIN  |
| 33         | 161.5 | 11.4        | 2319   | 1     | NTC3_RAT    |

|    |       |      |      |   |            |        |             |
|----|-------|------|------|---|------------|--------|-------------|
| 34 | 161   | 11.4 | 618  | 1 | DLI3_HUMAN | Q9nyj7 | homo sapien |
| 35 | 160.5 | 11.4 | 643  | 1 | CD93_RAT   | Q9et61 | rattus norv |
| 36 | 160.5 | 11.4 | 2531 | 1 | NTC1_RAT   | Q07008 | rattus norv |
| 37 | 160   | 11.3 | 2437 | 1 | NTC1_BRARE | P46530 | brachydanio |
| 38 | 159.5 | 11.3 | 407  | 1 | PAT_BOVIN  | P22457 | bos taurus  |
| 39 | 158.5 | 11.2 | 456  | 1 | PRTC_BOVIN | P00745 | bos taurus  |
| 40 | 157.5 | 11.2 | 379  | 1 | WIFI_MOUSE | Q9wua1 | mus musculu |
| 41 | 157   | 11.1 | 676  | 1 | PRTS_HUMAN | P07225 | homo sapien |
| 42 | 157   | 11.1 | 1221 | 1 | FBI2_MOUSE | P37889 | mus musculu |
| 43 | 156   | 11.1 | 649  | 1 | PRTS_MACMU | Q28520 | macaca mula |
| 44 | 156   | 11.1 | 1213 | 1 | JAG3_BRARE | Q90y54 | brachydanio |
| 45 | 155.5 | 11.0 | 4590 | 1 | FATH_HUMAN | Q14517 | homo sapien |

ALIGNMENTS

RESULT 1  
NTC4\_MOUSE STANDARD; PRT; 1964 AA.  
AC P1655; Q62389; Q62390; O35442; Q9RIW9; O88314; O88316; Q9RIK0;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-UN-2002 (Rel. 41, Last annotation update)  
DE Neogenetic locus notch homolog protein 4 precursor (Notch 4)  
DE [Contains: Transforming protein Int-3].  
GN NOTCH4 OR INT3 OR INT-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92194507; PubMed=1312643;  
RA Robbins J., Blondel B.J., Callahan D., Callahan R.;  
RT "Mouse mammary tumor gene int-3: a member of the notch gene family  
RT transforms mammary epithelial cells.";  
RL J. Virol. 66:2594-2599(1992).  
RN [2]  
RP REVISIONS, SEQUENCE FROM N.A.  
RX MEDLINE=97294599; PubMed=9150355;  
RA Callahan D., Callahan R.;  
RT "The mouse mammary tumor associated gene INT3 is a unique member of  
RT the NOTCH gene family (NOTCH4).";  
RN Oncogene 14:1883-1890(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Lung, and Testis;  
RC MEDLINE=96281668; PubMed=8681805;  
RA Uytendaele H., Marazzi G., Wu G., Yan Q., Saassoon D., Kitajewski J.;  
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial  
RT cell-specific mammalian Notch gene.";  
RL Development 122:2251-2259(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Rowen L., Mahairas G., Qin S., Ahern M.E., Dankers C., Laskey S.,  
RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackone K., Hood L.;  
RT "Sequence of the mouse major histocompatibility locus class III  
RT region.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1436-1600 FROM N.A.  
RX MEDLINE=99252212; PubMed=10233982;  
RA Lee J.-S., Hartung T., Ishimoto A., Honjo T., Yanagawa S.-I.;  
RT "Intracisternal type A particle-mediated activation of the Notch4/int3  
RT gene in a mouse mammary tumor: generation of truncated Notch4/int3  
RT mRNAs by retroviral splicing events.";  
RL J. Virol. 73:5166-5171(1999).  
RN [6]  
RP FUNCTION.  
RX MEDLINE=21244657; PubMed=11344305;  
RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;  
RT "Vascular patterning defects associated with expression of activated

RT Notch4 in embryonic endothelium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).  
 RN [7]  
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS  
 RP OF VAL-1463.  
 RA MEDLINE=21523956; PubMed=11518718;  
 RX Saxena M.T., Schroter E.H., Mumm J.S., Kopan R.;  
 RA "Murine notch homologs (NL-4) undergo presenilin-dependent  
 RT proteolysis.";  
 RL J. Biol. Chem. 276:40268-40273(2001).  
 RN [8]  
 RP POST-TRANSLATIONAL PROCESSING  
 RX MEDLINE=21374376; PubMed=11459941;  
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
 RA "Conservation of the biochemical mechanisms of signal transduction  
 RT among mammalian Notch family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity). May regulate branching  
 CC morphogenesis in the developing vascular system.  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart  
 CC kidney, and at lower levels in the ovary and skeletal muscle. A  
 CC very low expression is seen in the brain, intestine, liver and  
 CC testis.  
 CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during  
 CC embryonic development from 9.0 d.p.c.  
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane.  
 CC -!- PTM: Phosphorylated.  
 CC -!- DISEASE: Loss of the extracellular domain causes constitutive  
 CC activation of the Notch protein, which leads to hyperproliferation  
 CC of glandular epithelial tissues and development of mammary  
 CC carcinomas.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M80456; AAB38377.1; -;  
 CC EMBL; U43691; AAC52630.1; -;  
 CC EMBL; U43691; AAC52631.1; -;  
 CC EMBL; AF030001; AAB82004.1; -;  
 CC EMBL; AB016771; BAA32281.1; ALT SEQ.  
 CC EMBL; AB016772; BAA32283.1; ALT INIT.  
 CC EMBL; AB016773; BAA32284.1; ALT\_INIT.  
 CC EMBL; AB016774; BAA32285.1; -;

DR PIR: A38072; TMVMT3.  
 DR HSSP; P08709; IBF9.  
 DR MGD; MGI:107471; Notch4.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 27.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 2.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR00010; EGFBL00D.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_Ca; 11.  
 DR SMART; SM00001; EGF\_like; 15.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS00088; ANK\_REPEAT; 5.  
 DR PROSITE; PS02097; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 DR PROSITE; PS00022; EGF\_1; 28.  
 DR PROSITE; PS01186; EGF\_2; 21.  
 DR PROSITE; PS01187; EGF\_Ca; 9.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.  
 FT SIGNAL 1 20  
 FT CHAIN 21 1964  
 FT CHAIN 1411 1964  
 FT CHAIN 1428 1964  
 FT CHAIN 1463 1964  
 FT DOMAIN 21 1443  
 FT TRANSMEM 1444 1464  
 FT DOMAIN 1465 1964  
 FT DOMAIN 21 60  
 FT DOMAIN 61 112  
 FT DOMAIN 115 152  
 FT DOMAIN 153 189  
 FT DOMAIN 191 229  
 FT DOMAIN 231 271  
 FT DOMAIN 273 309  
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 FT DOMAIN 352 388  
 FT DOMAIN 389 427  
 FT DOMAIN 429 470  
 FT DOMAIN 472 508  
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 FT DOMAIN 548 584  
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 FT DOMAIN 688 724  
 FT DOMAIN 726 762  
 FT DOMAIN 764 800  
 FT DOMAIN 803 839  
 FT DOMAIN 841 877  
 FT DOMAIN 878 924  
 FT DOMAIN 926 962  
 FT DOMAIN 964 1000  
 FT DOMAIN 1002 1040  
 FT DOMAIN 1042 1081  
 FT DOMAIN 1083 1122  
 FT DOMAIN 1126 1167  
 FT REPEAT 1168 1208  
 FT REPEAT 1209 1242  
 FT REPEAT 1243 1282  
 FT REPEAT 1628 1657  
 FT REPEAT 1661 1691  
 FT REPEAT 1695 1724  
 FT REPEAT 1728 1757

Query Match 13.9%; Score 196; DB 1; Length 1964;  
 Best Local Similarity 34.2%; Pred. No. 1.9e-07;  
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

QY 61 APPRPRACCPGK-RTSLPGACGAIICPPPRNGSCYCPG---RCRCPRAGMDTQ 116  
 DB 134 ASGRPOSCSPGTGRCQQLRDCSA---NPCANGVCLATVPQIQCRCPGFEHGTCH 189  
 QY 117 SDVDECSARGGGPO--RCVNTGSGYWCOC---MEGHSLSADTGLVCP---KGPFRVA 167  
 DB 190 RDINECLFEPGPPQGTSCNNTGSIYQCLCPVQGBQCKLRKACPPSGCLNGTICQLV 249  
 QY 168 PNP-----TGVDANKKEE 180  
 DB 250 PEGHSTPHLCPCPGFTGLDCENMPD 275

RESULT 2  
 NTCH4 HUMAN STANDARD; PRT; 2003 AA.  
 AC 099466; 000306; 099940; 099458; 09H358; 09U119; 09U1J0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neogenic locus notch homolog protein 4 precursor (Notch 4)  
 DE (hncch4).  
 GN NOTCH4.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97311416; PubMed=9168133;  
 RA Sugaya K., Sasamura S.-I., Nohata J., Kimura T., Fukagawa T.,  
 Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;  
 "Gene organization of human NOTCH4 (CTG) n polymorphism in this  
 human counterpart gene of mouse proto-oncogene Int3.";  
 RT Gene 189:235-244 (1997).  
 RL Gene 189:235-244 (1997).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).  
 RC TISSUE=Bone marrow, and Heart;  
 RX MEDLINE=98360091; PubMed=9693032;  
 RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,  
 Friedman C., Chen L., Tresek B.J., Spies T., Rowen L., Hood L.;  
 "Cloning, characterization, and the complete 56.8-kilobase DNA  
 sequence of the human NOTCH4 gene.";  
 RT Genomics 51:45-58 (1998).  
 RL [3]  
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.  
 RA Miyagawa T., Tokunaga K., Hojo H.;  
 RT "Human notch4 gene variant.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 Banks A., Leitman J., Ward D., Ish-Horowitz D., Attavanas-Tsakonas S.;  
 "Human ligands of the Notch receptor.";  
 RT Am. J. Pathol. 154:785-794 (1999).  
 RL [5]  
 RL FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Deltal to regulate cell-fate determination.  
 Upon ligand activation through the released cell-fate determination  
 domain (NICD) it forms a transcriptional activator complex with  
 RBP-J kappa and activates genes of the enhancer of split locus.  
 Affects the implementation of differentiation, proliferation and  
 apoptotic programs. May regulate branching morphogenesis in the  
 developing vascular system (By similarity).  
 -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 terminal fragment N(EC) which are probably linked by disulfide  
 bonds (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in  
 CC the lung and placenta and at low levels in the liver, skeletal  
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow  
 CC and fetal liver. No expression was seen in adult brain or  
 CC peripheral blood leukocytes.  
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -1- PTM: Phosphorylated (By similarity).  
 CC -1- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal  
 CC peptide) is polymorphic and the number of Leu varies in the  
 CC population (from 6 to 12).  
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 1438 to 1463.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; D63395; BAA09708.1; ALT\_FRAME.  
 DR EMBL; D86566; BAA13116.1; -.  
 DR EMBL; U95299; AAC32288.1; -.  
 DR EMBL; U89335; AAC63097.1; -.  
 DR EMBL; AB023961; BAB20317.1; -.  
 DR EMBL; AB024520; BAA88951.1; -.  
 DR EMBL; AB024578; BAA88952.1; -.  
 DR HSSP; P08709; 1BF9.  
 DR Genew; HGNC:7884; NOTCH4.  
 DR MIM; 164951; -.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF\_1-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001338; EGF\_11.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 26.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 2.  
 DR PRINTS; PR00010; EGRBLDOD.  
 DR PRINTS; PR00011; EGFAMININ.  
 DR PRINTS; PR00012; ENTPEL.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_CA; 11.  
 DR SMART; SM00001; EGF\_Like; 15.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 5.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 DR PROSITE; PS00022; EGF\_1; 28.  
 DR PROSITE; PS01186; EGF\_2; 21.  
 DR PROSITE; PS01187; EGF\_CA; 9.  
 KW Receptor; Transcription regulation; Activator; Differentiation;



DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00001; EGF\_Like; 3.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWC; 2.  
 DR Glycoprotein; EGF-like domain; Repeat; Signal.  
 KM SIGNAL; 1 24  
 FT CHAIN; 25 816  
 FT DOMAIN; 30 258  
 FT DOMAIN; 272 331  
 FT DOMAIN; 332 396  
 FT DOMAIN; 397 439  
 FT DOMAIN; 440 481  
 FT DOMAIN; 482 522  
 FT DOMAIN; 521 553  
 FT DOMAIN; 555 601  
 FT DOMAIN; 602 637  
 FT DOMAIN; 638 693  
 FT DOMAIN; 698 756  
 FT DOMAIN; 758 813  
 FT DISULFID; 401 413  
 FT DISULFID; 407 422  
 FT DISULFID; 424 438  
 FT DISULFID; 444 457  
 FT DISULFID; 451 466  
 FT DISULFID; 468 480  
 FT DISULFID; 486 499  
 FT DISULFID; 493 508  
 FT DISULFID; 510 521  
 FT DISULFID; 525 535  
 FT DISULFID; 529 541  
 FT DISULFID; 543 552  
 FT DISULFID; 559 572  
 FT DISULFID; 566 581  
 FT DISULFID; 583 600  
 FT DISULFID; 606 619  
 FT DISULFID; 613 628  
 FT DISULFID; 630 636  
 FT CARBOHYD; 53 53  
 FT CARBOHYD; 225 225  
 FT CARBOHYD; 293 293  
 FT CARBOHYD; 298 298  
 FT CARBOHYD; 517 517  
 FT CARBOHYD; 615 615  
 FT CARBOHYD; 635 635  
 SQ SEQUENCE 816 AA; 91163 MW; SBD0A946F87E7AD CRC64;  
 Query Match 13.0%; Score 184; DB 1; Length 816;  
 Best Local Similarity 28.8%; Pred. No. 6; Ge-07;  
 Matches 46; Conservative 22; Mismatches 64; Indels 28; Gaps 7;  
 QY 7 PGRRAVRAHGDPSSEFVQVYVQPLT---CDGRACSTYRTIYRVRSGPLAPA 63  
 DB 461 PGSEFVCVCKT-GYIRIDYSCHEDECLTQHNDENALC--PNTV-----G 504  
 QY 64 RPRYACPGMRTSGLPACAAICQPPCRNGSCVOPGRCRCPAGMRGDTQGVDECS 123  
 DB 505 GHNCKCKGTYGN-----GTTCKAFCKDCRCNGACAIANVACAPQGFPGSCETIDEC 560  
 QY 124 ARGGCPOR--CVNTAGSYVQCWEGHSLADGTLGVCKG 161  
 DB 561 EGFVQCDSPRANCIINLPGWYHCECRDGYH--DNGMFAPGG 597

AC Q92832; Q9Y472;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1)  
 DE (Nel-related protein 1).  
 GN NELL1 OR NRPL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97131504; PubMed=8975702;  
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;  
 RT "Cloning and characterization of two novel human cDNAs (NELL1 and  
 RL NELL2) encoding proteins with six EGF-like repeats.";  
 RL Genomics 38:273-276(1996).  
 RP SEQUENCE OF 383-810 FROM N.A.  
 RA Ting K., Vastardis H., Mulliken J.B., Bertolami C., Wen Z.,  
 RA Young M., Tieu A., Kwong E.;  
 RT "Nel homolog gene expression in craniofacial anomalies.";  
 RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -1-SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1-DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.  
 CC -1-SIMILARITY: CONTAINS 5 VWC DOMAINS.  
 CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -1-CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS  
 IN POSITIONS 427 AND 771.  
 CC  
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 CC  
 CC EMBL; D83017; BAAL1680.1; -  
 CC EMBL; U57523; AAB06946.1; ALT\_FRAME.  
 CC HSSP; P07204; IADX.  
 CC Genew; HGNC:7750; NELL1.  
 DR MIM: 602319; -  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF\_Like.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWC\_C.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00001; EGF\_Like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWC; 2.  
 KM Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL; 1 16  
 FT CHAIN; 17 810  
 FT DOMAIN; 81 230  
 FT DOMAIN; 273 331  
 FT DOMAIN; 335 390  
 FT VWC 1.  
 FT VWC 2.

FT DOMAIN 391 433  
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 FT DOMAIN 515 547  
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 FT DOMAIN 692 750  
 FT DOMAIN 752 807  
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 FT DISULFID 418 432  
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 FT DISULFID 480 493  
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 FT DISULFID 553 566  
 FT DISULFID 560 575  
 FT DISULFID 577 594  
 FT DISULFID 600 613  
 FT DISULFID 607 622  
 FT DISULFID 624 630  
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 FT CARBOHYD 53 53  
 FT CARBOHYD 83 83  
 FT CARBOHYD 224 224  
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 FT CARBOHYD 511 511  
 FT CARBOHYD 562 562  
 FT CARBOHYD 609 609  
 FT CARBOHYD 708 708  
 FT CARBOHYD 732 732  
 FT CARBOHYD 758 758  
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 FT CONFLICT 626 626  
 SQ SEQUENCE 810 AA; 89606 MW; 549465EA3F7AEED0 CRC64;

Query Match 13.0%; Score 183; DB 1; Length 810;  
 Best Local Similarity 38.5%; Pred. No. 7.8e-07;  
 Matches 37; Conservative 11; Mismatches 38; Indels 10; Gaps 3;

QY 69 CPGWKRTSGLPGACGAI C P P C R N G S G C V P G R C R C P A G W R G D T C Q S D V D E C S A R R G G 128  
 Db 504 KPGVGN-----GTTCRAFCEGCRVGTGTCVAPNKCVCPSGFTGSHCEKIDECSEGIIE 559  
 QY 129 C--PQRCVNTAGSWCQWEGH-----SLSDAGTGLCV 158  
 Db 560 CHNHSRCVNLPGWYHCECRSGFHDHDTYSLSGSCI 595

RESULT 5  
 ID\_NEL2 HUMAN STANDARD; PRT; 816 AA.  
 AC Q99435;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE protein kinase C-binding protein NELL2 precursor (NEL-like protein 2)  
 DE (Nel-related protein 2).  
 GN NELL2 OR NRP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

TISSUE=Brain;  
 MEDLINE=97131504; PubMed=8975702;  
 Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.,  
 "Cloning and characterization of two novel human cDNAs (NELL1 and  
 NELL2) encoding proteins with six EGF-like repeats.",  
 Genomics 38:273-276(1996).  
 [2]  
 TSP N-TERMINAL DOMAIN.  
 MEDLINE=98153258; PubMed=9480764;  
 Beckmann G., Hanke J., Bork P., Reich J.;  
 "Merging extracellular domains: fold prediction for laminin G-like  
 and amino-terminal thrombospondin-like modules based on homology to  
 pentraxins.",  
 J. Mol. Biol. 275:725-730(1998).  
 CC -!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL: D83018; BAA11681.1; -.  
 HSP: P00740; IEDM.  
 Genew; HGNC:7751; NELL2.  
 MIM; 6023320; -.  
 InterPro: IPR000152; Asx hydroxyl.  
 InterPro: IPR000561; EGF-like.  
 InterPro: IPR001881; EGF Ca.  
 InterPro: IPR001791; Laminin\_G.  
 InterPro: IPR003129; TSPN.  
 InterPro: IPR001007; VWF C.  
 Pfam: PF00008; EGF; 5.  
 Pfam: PF00093; VWC; 3.  
 Pfam: PF02210; TSPN; 1.  
 SMART; SM00179; EGF CA; 3.  
 SMART; SM00001; EGF\_Like; 3.  
 SMART; SM00282; LamG; 1.  
 SMART; SM00210; TSPN; 1.  
 SMART; SM00214; VWC; 3.  
 PROSITE; PS00010; ASX HYDROXYL; 3.  
 PROSITE; PS00022; EGF\_1; 1.  
 PROSITE; PS01186; EGF\_2; 4.  
 PROSITE; PS01187; EGF\_CA; 3.  
 PROSITE; PS01208; VWFC; 2.  
 Glycoprotein; EGF-like domain; Repeat; Signal.  
 SIGNAL 1 24  
 POTENTIAL.  
 CHAIN 25 816  
 DOMAIN 30 258  
 TSP N-TERMINAL.  
 VWFC 1.  
 VWFC 2.  
 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).  
 EGF-LIKE 2.  
 EGF-LIKE 3.  
 EGF-LIKE 4.  
 EGF-LIKE 5.  
 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).  
 VWFC 3.  
 VWFC 4.  
 VWFC 5.  
 BY SIMILARITY.  
 DISULFID 401 413  
 BY SIMILARITY.  
 DISULFID 407 422  
 BY SIMILARITY.  
 DISULFID 424 438  
 BY SIMILARITY.  
 DISULFID 444 457  
 BY SIMILARITY.  
 DISULFID 451 466  
 BY SIMILARITY.  
 DISULFID 468 480



FT DISULFID 486 499 BY SIMILARITY.  
 FT DISULFID 493 508 BY SIMILARITY.  
 FT DISULFID 510 521 BY SIMILARITY.  
 FT DISULFID 525 535 BY SIMILARITY.  
 FT DISULFID 529 541 BY SIMILARITY.  
 FT DISULFID 543 552 BY SIMILARITY.  
 FT DISULFID 559 572 BY SIMILARITY.  
 FT DISULFID 583 600 BY SIMILARITY.  
 FT DISULFID 606 619 BY SIMILARITY.  
 FT DISULFID 613 628 BY SIMILARITY.  
 FT DISULFID 630 636 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 816 AA; 91346 MW; 89370B987DC7A324 CRC64;

Query Match 12.8%; Score 181.5; DB 1; Length 816;  
 Best Local Similarity 36.8%; Pred. No. 1e-06; Indels 9; Gaps 3;  
 Matches 35; Conservative 14; Mismatches 37;

QY 69 CCGPCKRTSGLPACGAICPPPCRGSCVCPGRCPCAGWRGDTQSDVDECSARRGG 128  
 DB 510 CKPYTGN---GTTCKAFCKDGRNGACIAAVCACPGFTGSPCETDIDECSDGFVQ 565  
 QY 129 CPQR--CVNTAGSYWCQCGWEGHSLADGTLCPKG 161  
 DB 566 CDSRANCINLPGWYHCECRDGYH--DNGMFSPSG 597

RESULT 6  
 ID NEIL RAT STANDARD; PRT; 810 AA.

AC 062919;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein Kinase C-binding protein NEIL1 precursor (NEIL-like protein 1).  
 GN NEIL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 [1]  
 RA SEQUENCE FROM N.A.  
 RX STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=20017976; Pubmed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 Abe T., Matsubashi S., Ting K.;  
 "Biochemical characterization and expression analysis of neural  
 chromospondin-1-like proteins NEIL1 and NEIL2."  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 CC -1 SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 5 WFPC DOMAINS.  
 CC -1 SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL; U48246; AAC72252.1; -;  
 DR HSSP; P35555; IEMN.  
 DR InterPro; IPR000152; Aex\_hydroxyl.

DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; WFC\_C.  
 DR Pfam; PF00068; EGF; 4.  
 DR Pfam; PF00093; WFC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_Ca; 2.  
 DR SMART; SM00001; EGF\_Like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; WFC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_Ca; 3.  
 DR PROSITE; PS01208; WFC; 2.  
 DR Glycoprotein; EGF-like domain; Repeat; Signal.  
 KW SIGNAL  
 FT CHAIN 1 16  
 FT DOMAIN 17 810  
 FT DOMAIN 81 230  
 FT DOMAIN 273 331  
 FT DOMAIN 335 390  
 FT DOMAIN 391 433  
 FT DOMAIN 434 475  
 FT DOMAIN 476 515  
 FT DOMAIN 515 547  
 FT DOMAIN 549 595  
 FT DOMAIN 596 631  
 FT DOMAIN 632 687  
 FT DOMAIN 692 750  
 FT DOMAIN 752 807  
 FT DISULFID 395 407  
 FT DISULFID 401 416  
 FT DISULFID 418 432  
 FT DISULFID 438 451  
 FT DISULFID 445 460  
 FT DISULFID 462 474  
 FT DISULFID 480 493  
 FT DISULFID 487 502  
 FT DISULFID 504 515  
 FT DISULFID 519 529  
 FT DISULFID 523 535  
 FT DISULFID 537 546  
 FT DISULFID 553 566  
 FT DISULFID 560 575  
 FT DISULFID 577 594  
 FT DISULFID 600 613  
 FT DISULFID 607 622  
 FT DISULFID 624 630  
 FT CARBOHYD 40 40  
 FT CARBOHYD 53 53  
 FT CARBOHYD 83 83  
 FT CARBOHYD 224 224  
 FT CARBOHYD 224 294  
 FT CARBOHYD 372 372  
 FT CARBOHYD 372 372  
 FT CARBOHYD 511 511  
 FT CARBOHYD 562 562  
 FT CARBOHYD 609 609  
 FT CARBOHYD 708 708  
 SQ SEQUENCE 810 AA; 89212 MW; 46F09C466AF9AB0B CRC64;

Query Match 12.8%; Score 181; DB 1; Length 810;  
 Best Local Similarity 37.5%; Pred. No. 1e-06;  
 Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 69 CCGPCKRTSGLPACGAICPPPCRGSCVCPGRCPCAGWRGDTQSDVDECSARRGG 128  
 DB 504 CCGYVGN---GTTCKAFCKDGRNGACIAAVCACPGFTGSPCETDIDECSDGFVQ 559  
 QY 129 CP--QR--CVNTAGSYWCQCGWEGH---SLADGTLCPV 158

Db 560 CHNYSRCVNLPGWYHCECRSGFDDGTYSLSGESCI 595

## RESULT 7

NEL2 RAT  
ID NEL2 RAT STANDARD; PRT; 816 AA.  
AC Q62918;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein kinase C-binding protein NELL2 precursor (NEL-like protein 2).  
GN NELL2 OR NEL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAINS=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=20017976; PubMed=10548494;  
RA Kuroda S., Oyasu W., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
RA Abe T., Matsushashi S., Ting K.;  
RT "Biochemical characterization and expression analysis of neural  
thrombospondin-1-like proteins NELL1 and NELL2.";  
RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
RN [2]  
RP TSP N-TERMINAL DOMAIN.  
RX MEDLINE=98153258; PubMed=9480764;  
RA Beckmann G., Hanke J., Bork P., Reich J.;  
RT "Merging extracellular domains: fold prediction for laminin G-like  
and amino-terminal thrombospondin-like modules based on homology to  
pentraxins.";  
RL J. Mol. Biol. 275:725-730(1998).  
CC -!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
CC -!- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
CC -!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U48245; AAC72245.1; -.  
DR HSSP; P00740; 1EDM.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR003129; TSPN.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF00093; VWC; 3.  
DR Pfam; PF02210; TSPN; 1.  
DR SMART; SM00179; EGF\_CA; 3.  
DR SMART; SM00001; EGF\_like; 3.  
DR SMART; SM00282; LamG; 1.  
DR SMART; SM00210; TSPN; 1.  
DR SMART; SM00214; VWC; 3.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS01187; EGF\_CA; 3.  
DR PROSITE; PS01208; VWFC; 2.  
KW Glycoprotein; EGF-like domain; Repeat; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 816 PROTEIN KINASE C-BINDING PROTEIN NELL2.  
FT DOMAIN 30 258 TSP N-TERMINAL.  
FT DOMAIN 272 331 VWFC 1.

FT DOMAIN 332 396  
FT DOMAIN 397 439  
FT DOMAIN 440 481  
FT DOMAIN 482 522  
FT DOMAIN 521 553  
FT DOMAIN 555 601  
FT DOMAIN 602 637  
FT DOMAIN 638 693  
FT DOMAIN 698 756  
FT DOMAIN 758 813  
FT DISULFID 401 413  
FT DISULFID 407 422  
FT DISULFID 424 438  
FT DISULFID 444 457  
FT DISULFID 451 466  
FT DISULFID 468 480  
FT DISULFID 486 499  
FT DISULFID 493 508  
FT DISULFID 510 521  
FT DISULFID 525 535  
FT DISULFID 529 541  
FT DISULFID 543 552  
FT DISULFID 559 572  
FT DISULFID 566 581  
FT DISULFID 583 600  
FT DISULFID 606 619  
FT DISULFID 613 628  
FT DISULFID 630 636  
FT CARBOHYD 25 53  
FT CARBOHYD 225 235  
FT CARBOHYD 233 293  
FT CARBOHYD 298 298  
FT CARBOHYD 517 517  
FT CARBOHYD 615 615  
FT CARBOHYD 635 635  
SQ SEQUENCE 816 AA; 90952 MW; A999F76078060D6B CRC64;  
Query Match 12.7%; Score 179.5; DB 1; Length 816;  
Best Local Similarity 35.8%; Pred. No. 1.5e-06;  
Matches 34; Conservative 15; Mismatches 37; Indels 9; Gaps 3;  
QY 69 CPGKWKRTSGLPGACAAICQPPCRNGGSCVQPGRCRCPCAGWRGDTCCSDVDVDCSARRGG 128  
Db 510 CKEGYTGN---GTTCCKAFCKDCKNGACIAANVCAPQSGFTGPGSCETIDECSEGVQ 565  
QY 129 CPQR--CVNTAGSYWCQWEGHSLSDGTLCVPKG 161  
Db 566 CDSRANCINLPGWYHCECRDGVH---DNGMFAPGG 597  
RESULT 8  
CD93\_HUMAN  
ID CD93\_HUMAN STANDARD; PRT; 652 AA.  
AC Q9NFY3; O00274;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement component C1q receptor precursor (Complement component 1, q  
subcomponent, receptor 1) (C1qr) (C1qR(p)) (C1q/MBL/SPA receptor)  
DE (CD93 antigen) (CDW93).  
GN C1QR1 OR CD93.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX PubMed=9047234;  
RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;  
RT "cDNA cloning and primary structure analysis of C1qR(p), the human  
C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";  
RL Immunity 6:119-129(1997).  
RN [2]

RP SEQUENCE FROM N.A., AND VARIANT ALA-318.  
 RX PubMed=11781389;  
 RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,  
 RA Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;  
 RT "Identification of human CD93 as the phagocytic C1q receptor (C1qR)  
 by expression cloning";  
 RL J. Leukoc. Biol. 71:133-140(2002).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21638749; PubMed=11780052;  
 RX Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.W., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grainger D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalho M.H., Liversidge M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurtry A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,  
 RA Swann R.M., Symons N., Taylor R., Tee L., Thomas J.W., Thorpe A.,  
 RA Tracey A., Tyromans A.C., Vaudin R., Wall M., Wallis J.W.,  
 RA Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Leukocyte;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 [5]  
 RN CHARACTERIZATION.  
 RX PubMed=11994479;  
 RA McGreal E.P., Ikegaki N., Akatsu H., Morgan B.P., Gasque P.;  
 RT "Human C1qR is identical with CD93 and the mfi-11 antigen but does  
 not bind C1q";  
 RL J. Immunol. 168:5222-5232(2002).  
 [6]  
 RN O-GLYCOSYLATION.  
 RX PubMed=10092817;  
 RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;  
 RT "C1qR is a heavily O-glycosylated cell surface protein involved in  
 the regulation of phagocytic activity";  
 RL J. Immunol. 162:3583-3589(1999).  
 [7]  
 RN FUNCTION: Receptor (or element of a larger receptor complex) for  
 C1q, mannose-binding lectin (MBL2) and pulmonary surfactant  
 protein A (SPA). May mediate the enhancement of phagocytosis in  
 monocytes and macrophages upon interaction with soluble defense  
 collagens. May play a role in intercellular adhesion.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,  
 platelets, cells of myeloid origin, such as monocytes and  
 neutrophils. Not expressed in cells of lymphoid origin.  
 CC -1- PTM: N- and O-glycosylated.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.  
 CC -1- CAUTION: Has been sometimes referred to as a collectin receptor.  
 CC -1- CAUTION: According to Ref.5, C1q is not a ligand for C1QR1.  
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);  
 WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456\_g.htm".

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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; U94333; AAB53110.1; -  
 CC EMBL; AL118508; CAC00597.1; -  
 CC EMBL; BC028075; AAH28075.1; -  
 CC HSSP; P35555; IEMN.  
 CC MIM; 120577; -  
 CC InterPro; IPR000152; Aax\_hydroxy1.  
 CC InterPro; IPR000561; EGF\_Like.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR001304; Lectin\_C.  
 CC InterPro; IPR001187; Tissue\_factor.  
 CC Pfam; PF00008; EGF; 5.  
 CC Pfam; PF00059; Lectin\_C; 1.  
 CC Pfam; PF01108; Tissue\_fac; 1.  
 CC SMART; SM00034; CLECT; 1.  
 CC SMART; SM00179; EGF\_CA; 3.  
 CC SMART; SM00001; EGF\_Like; 2.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 3. FALSE\_NEG.  
 CC PROSITE; PS00615; C-TYPE LECTIN\_1; 1.  
 CC PROSITE; PS00041; C-TYPE LECTIN\_2; 1.  
 CC PROSITE; PS01186; EGF\_2; 3.  
 CC PROSITE; PS01187; EGF\_CA; 3.  
 CC Receptor; EGF-like domain; Signal; Transmembrane; Glycoprotein;  
 CC Repeat; Lectin; Polymorphism.  
 CC SIGNAL 1 21  
 CC CHAIN 22 652  
 CC DOMAIN 24 580  
 CC TRANSMEM 581 601  
 CC DOMAIN 602 652  
 CC DOMAIN 32 174  
 CC DOMAIN 32 301  
 CC DOMAIN 302 344  
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 CC CONFLICT 38 39 TA -> T (IN AA SEQUENCE).  
 CC CONFLICT 155 155 TA -> N (IN REF. 1).  
 CC CONFLICT 186 186 G -> A (IN AA SEQUENCE).  
 CC CONFLICT 492 492 S -> A (IN AA SEQUENCE).  
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 Query Match 12.5%; Score 176; DB 1; Length 652;



ID FBN1 HUMAN STANDARD; PRT; 2871 AA.  
 AC P35555;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBN1 OR FBN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=93372860; PubMed=8364578;  
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,  
 Pangillan T., Bonadio J.;  
 RT "Genomic organization of the sequence coding for fibrillin, the  
 RT defective gene product in Marfan syndrome.";  
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 RC TISSUE=Placenta, and Fibroblast;  
 RX MEDLINE=94010947; PubMed=7691719;  
 RA Corson G.M., Chabberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;  
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 RT multidomain structure and alternatively spliced exons at the 5'  
 RT end.";  
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 RN RP SEQUENCE OF 899-2871 FROM N.A.  
 RX MEDLINE=91304568; PubMed=1852207;  
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 RN RP STRUCTURE BY NMR OF 2054-2125.  
 RX MEDLINE=98031893; PubMed=9362480;  
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 RN RP STRUCTURE BY NMR OF 2124-2205.  
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 RN RP VARIANT MFS PRO-1137.  
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 RN RP VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.  
 RX MEDLINE=94108431; PubMed=8281141;  
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VARIANT MFS CYS-627.  
MEDLINE=94272487; PubMed=8004112;  
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syndrome patients";  
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VARIANT MFS CYS-122.  
MEDLINE=94314977; PubMed=8040326;  
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variant of Marfan syndrome.";  
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VARIANT MFS TYR-1223.  
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syndrome";  
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VARIANT MFS HIS-1170.  
MEDLINE=95174777; PubMed=7870075;  
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arachnodactyly";  
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[24]  
VARIANTS MFS G-2117; N-1023; R-1074; Y-1242; E-2127; W-2151;  
K-2447 AND R-2511.  
MEDLINE=94184368; PubMed=8136837;  
RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;  
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[25]  
VARIANT SER-1127.  
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Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;  
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DB 54 KGNVCGSRYNAYCCFGWKT---LFGGNQCIYVICHSBGDFCSRPNMCTCPSQIAPS 110  
QY 83 -----CGAICQPPNRNGSCVQPCRCPA 108  
DB 111 CGSRSIQHCNIRCMNGSGSCDDHCLCQKGYIGTHGQFPVCSGCLNGRCVAPNRCACTY 170  
QY 109 GWRGDTCC----- 116  
DB 171 GFTGPOCERDYRTGPGFTVISNMQCGQLSGIVCTKQLCCATVGRAGWPCMCQAQHP 230  
QY 117 -----SDVDCSARRGCGP-QRCVNTAGSYWCQWEGHLSADGTLG----- 157

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DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Fibrillin 2 precursor.  
GN FBN2 OR FBN-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
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RP SEQUENCE FROM N.A.  
RX MEDLINE=95263670; PubMed=7744963;  
RA Zhang H., Hu W., Ramirez F.;  
RT "Developmental expression of fibrillin genes suggests heterogeneity  
of extracellular microfibrils";  
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RP SEQUENCE OF 210-317 FROM N.A.  
RX MEDLINE=94140368; PubMed=8307578;  
RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
RA Francke U.;  
RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
mouse chromosomes 2 and 18";  
RL Genomics 18:667-672 (1993).  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DB EMBL; L39790; AAA74908.1; -  
DR EMBL; S69359; AAC60685.1; -  
DR HSSP; P35555; 1EMN.  
DR MGD; MGI:95490; Fbn2.  
DR InterPro; IPR000152; Asx hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF Ca.  
DR InterPro; IPR001438; EGF II.  
DR InterPro; IPR002212; Fibril-assoc.  
DR Pfam; PF00008; EGF; 46.  
DR Pfam; PF00683; TB; 9.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00179; EGF CA; 43.  
DR SMART; SM00001; EGF-like; 3.  
DR PROSITE; PS00010; ASX HYDROXYL; 43.  
DR PROSITE; PS00022; EGF\_1; 2.  
DR PROSITE; PS01186; EGF\_2; 36.  
DR PROSITE; PS01187; EGF CA; 43.  
DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
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FT CHAIN 29 2907  
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FT DOMAIN 145 176

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| FT | DOMAIN   | 176  | 208  | EGF-LIKE 3.                    |
| FT | DOMAIN   | 276  | 317  | EGF-LIKE 4, CALCITUM-BINDING.  |
| FT | DOMAIN   | 318  | 359  | EGF-LIKE 5, CALCITUM-BINDING.  |
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| FT | DOMAIN   | 487  | 527  | EGF-LIKE 6.                    |
| FT | DOMAIN   | 528  | 567  | EGF-LIKE 7, CALCITUM-BINDING.  |
| FT | DOMAIN   | 568  | 609  | EGF-LIKE 8, CALCITUM-BINDING.  |
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| FT | DOMAIN   | 1066 | 1107 | EGF-LIKE 15, CALCITUM-BINDING. |
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| FT | DISULFID | 1412 | 1427 | BY SIMILARITY. |
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| FT | DISULFID | 1529 | 1540 | BY SIMILARITY. |
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Query Match 12.4%; Score 175; DB 1; Length 2907;  
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 Db 94 HSYCCPGMKTLPGSNQCVLPICRNSCGDGFCSR---PIMCTSSGQGISPTGKRISIQCS 150  
 Oy 54 YRRSPGLAPARRRYVACPGWKRTSGLPACGAAICQPPCRNGSCVQPGRCRCPAGWRGD 113

Db 151 VRCWNGTTCADHHCQCKGYIGT-----YCGQPVCECNGGRCGIPNRCACVYGTGP 205  
 Qy 114 TCQ-----YCGQPVCECNGGRCGIPNRCACVYGTGP 205  
 Db 206 QCRDYRTGPGFTQVNNQMCQGLTGIVCTKLCATIGRANGHPCEMCPAQPCRP 265  
 Qy 117 -----SDVDECSARRGCP-ORCVNTAGSYWOCWGHSLSDGTLIC 157  
 Db 266 IPNIRTAGQDVDECAIPGLCGGNCINTVGSPECRCPAGHKQSETTKQC 316

RESULT 12  
 NTC3 HUMAN  
 ID NTC3 HUMAN STANDARD; PRT; 2321 AA.  
 AC Q9UM47; Q9Y6L8; Q9UPL3; Q9UEB3;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).  
 GN NOTCH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97032728; PubMed=8878478;  
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,  
 RA Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J.,  
 RA Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,  
 RA Bach J.-F., Bousser M.-G., Tournier-Lasserre E.;  
 RA "Notch3 mutations in CADASIL, a hereditary adult-onset condition  
 RA causing stroke and dementia.";  
 RT Nature 383:707-710(1996).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP Guel M., Artavanis-Teakonas S.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Lamerding J.E., McCready P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,  
 RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,  
 RA Frankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
 RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,  
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,  
 RA Carrano A.V.;  
 RA "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in  
 RT 19p13.1.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP VARIANTS CADASIL Y-49; C-71; C-90; C-110; C-133; C-141; R-146; C-153;  
 RP C-169; C-171; C-182; R-185; S-212; G-222; Y-224; C-258; Y-542; C-558;  
 RP C-578; C-728; C-985; C-1006; C-1031; C-1231 AND R-1261, AND VARIANTS  
 RP R-170; L-496; Q-1133; M-1183 AND A-2223.  
 RX MEDLINE=98049753; PubMed=9388399;  
 RA Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H.,  
 RA Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,  
 RA Bach J.-F., Tournier-Lasserre E.;  
 RA "Strong clustering and stereotyped nature of Notch3 mutations in  
 RT CADASIL patients.";  
 RL Lancet 350:1511-1515(1997).  
 RN [5]  
 RP VARIANT CADASIL 114-GLY--PRO-120 DEL.  
 RX MEDLINE=20264473; PubMed=10802807;  
 RA Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,  
 RA Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;  
 RT "Splice site mutation causing a seven amino acid Notch3 in-frame  
 RT deletion in CADASIL.";  
 RL Neurology 54:1874-1875(2000).  
 RN [6]

RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.,  
 RT "Human ligands of the Notch receptor.";  
 RL Am. J. Pathol. 154:785-794(1999).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity).  
 CC SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult  
 CC tissues.  
 CC -!- PM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -!- PM: Phosphorylated (By similarity).  
 CC -!- DISEASE: Defects in NOTCH3 are associated with CADASIL (Cerebral  
 CC autosomal dominant arteriopathy with subcortical infarcts and  
 CC leukoencephalopathy) which causes a type of stroke and dementia of  
 CC which key features include recurrent subcortical ischemic events  
 CC and vascular dementia.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; U97669; AAB91371.1; -;  
 DR EMBL; AF058900; AAC14346.1; -;  
 DR EMBL; AF058881; AAC14346.1; JOINED.  
 DR EMBL; AF058882; AAC14346.1; JOINED.  
 DR EMBL; AF058883; AAC14346.1; JOINED.  
 DR EMBL; AF058884; AAC14346.1; JOINED.  
 DR EMBL; AF058885; AAC14346.1; JOINED.  
 DR EMBL; AF058886; AAC14346.1; JOINED.  
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 DR EMBL; AC004257; AAC04897.1; -;  
 DR EMBL; AC004663; AAC15789.1; ALT\_INIT.





DR EMBL; X84822; CAA57709.1; JOINED.  
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 DR PIR; A33322; MMHUND.  
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 DR Genew; HGNC:7821; NID.  
 DR MIM; 131390; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR000033; Ldl\_receptor\_rep.  
 DR InterPro; IPR003886; Nidogen ext.  
 DR InterPro; IPR000716; Thyroglobulin\_1.  
 DR Pfam; PF00008; EGF; 6.  
 DR Pfam; PF00058; ldl\_recept\_b; 3.  
 DR Pfam; PF00086; thyroglobulin\_1; 1.  
 DR SMART; SM00179; EGF CA; 2.  
 DR SMART; SM00001; EGF-like; 4.  
 DR SMART; SM00135; LY; 5.  
 DR SMART; SM00533; NIDO; 1.  
 DR SMART; SM00211; TY; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
 DR PROSITE; PS00022; EGF 1; 1.  
 DR PROSITE; PS01186; EGF 2; 5.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
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 KW Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.  
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 FT CHAIN 29 1247 NIDOGN.  
 FT DOMAIN 29 669 I (LARGER GLOBULAR DOMAIN).  
 FT DOMAIN 670 917 II (CYSTEINE-RICH).  
 FT DOMAIN 918 1247 III (SMALLER GLOBULAR DOMAIN).  
 FT DOMAIN 386 426 EGF-LIKE 1.  
 FT DOMAIN 668 709 EGF-LIKE 2.  
 FT DOMAIN 710 751 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 758 801 EGF-LIKE 4.  
 FT DOMAIN 802 840 EGF-LIKE 5.  
 FT DOMAIN 872 919 EGF-LIKE 6.  
 FT DOMAIN 989 1030 THYROGLOBULIN TYPE 1.  
 FT DOMAIN 1032 1073 LDL-RECEPTOR YWTD MOTIF 1.  
 FT DOMAIN 1075 1118 LDL-RECEPTOR YWTD MOTIF 2.  
 FT DOMAIN 1124 1163 LDL-RECEPTOR YWTD MOTIF 3.  
 FT DOMAIN 1208 1244 LDL-RECEPTOR YWTD MOTIF 4.  
 FT MOD\_RES 289 289 EGF-LIKE 6.  
 FT MOD\_RES 296 296 SULFATION (POTENTIAL).  
 FT DISULFID 672 685 SULFATION (POTENTIAL).  
 FT DISULFID 672 685 BY SIMILARITY.  
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 FT DISULFID 762 777 BY SIMILARITY.  
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FT DISULFID 1219 1232 BY SIMILARITY.  
 FT DISULFID 1234 1243 BY SIMILARITY.  
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 FT CARBOHYD 1137 1137 N-LINKED (GLCNAC. .) (POTENTIAL).  
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 FT CONFLICT 37 42 FPGQG -> SAPDR (IN REF. 2).  
 FT CONFLICT 1115 1115 H -> T (IN REF. 3).  
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 Best Local Similarity 25.8%; Pred. No. 64e-06;  
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 DB 681 TNAACRFPRTQFTCECSIGFRGDRGTCYDIDECSE-----QP--SVGSHITCNH-- 730  
 QY 48 TIYRTAYRRSPGLAPARPRVACCPGKRTSGLPGACGAICQPP-----CRNG----- 95  
 DB 731 -----PGTFRCECEVEGYQFSD--EGTCVAVVDQRPINCYETGLHNCIDIPOR 774  
 QY 96 GSCVQPG-----RCRCPAGMRGD--TCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEHGS 149  
 DB 775 AQCIYTGSSSYTCSCLEPGFSGDQACQ--DVDECPQSRCHPDACFYNTPGSFTCQCKPFI-- 832  
 QY 150 LSADGTLCLVP-----KGGPRVAPNPTG----- 172  
 DB 833 -QGDGFRCPVEGEVETKRCQHEREHILGAAGATDPQPIPGFLFVPCDAHGHYAPTQCHG 891  
 QY 173 -----VDSAMKEEVQRLQSRVLLLEKQLVLAPLH--SLASQALEHGLPPGSLLVHS 224  
 DB 892 STGYCWCDRDGR--EVEGTRTRPGMTTCLSTVAPPPIHQGPVAVTAVIPLP--PGTHLL--- 947  
 QY 225 FOQLGRIDSL 234  
 DB 948 FAQTGKIERL 957  
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 AC Q01705; Q9058; Q99JC2; Q06007; Q61905; Q990X7;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 13-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A) (mt14) (p300).  
 DE NOTCH1 OR MOTCH.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
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 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Embryo;  
 RX MEDLINE=93194170; PubMed=8449489;  
 RA Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A., Copeland N.G., Gridley T.;  
 RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";  
 RL Genomics 15:259-264(1993).  
 RN [2]  
 RP SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.  
 RC STRAIN=CD-1; TISSUE=Embryo;  
 RX MEDLINE=93050801; PubMed=1426644;  
 RA Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;  
 RT "Expression analysis of a Notch homologue in the mouse embryo.";  
 RL Dev. Biol. 154:377-387(1992).  
 RN [3]  
 RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93048835; PubMed=1425352;  
 RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,





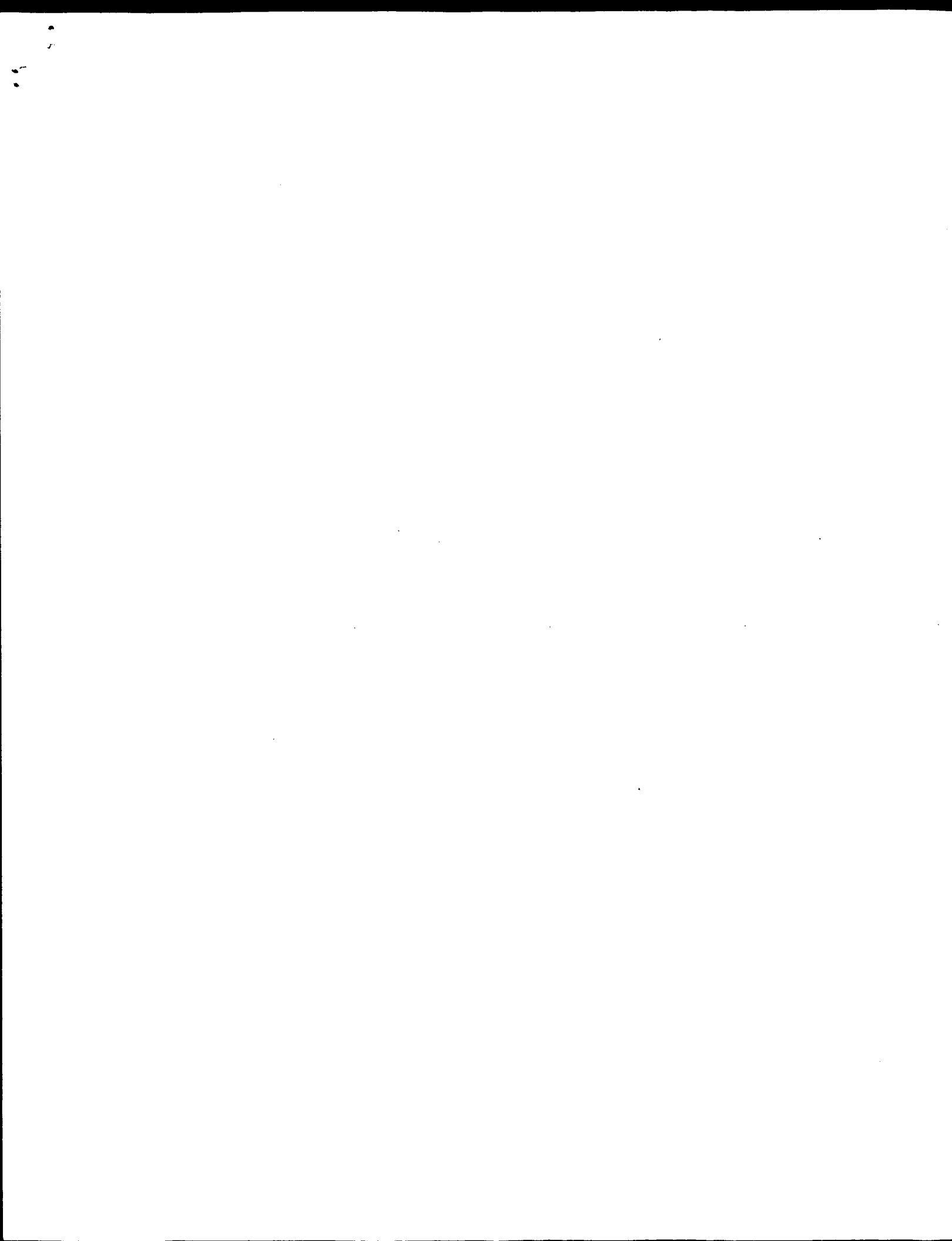
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| FT | DISULFID | 1415 | 1429 | BY SIMILARITY. |
| FT | DISULFID | 1431 | 1444 | BY SIMILARITY. |
| FT | DISULFID | 1450 | 1461 | BY SIMILARITY. |
| FT | DISULFID | 1456 | 1470 | BY SIMILARITY. |
| FT | DISULFID | 1472 | 1485 | BY SIMILARITY. |
| FT | DISULFID | 1491 | 1502 | BY SIMILARITY. |
| FT | DISULFID | 1497 | 1511 | BY SIMILARITY. |
| FT | DISULFID | 1513 | 1526 | BY SIMILARITY. |
| FT | DISULFID | 1510 | 1622 | BY SIMILARITY. |
| FT | DISULFID | 1617 | 1631 | BY SIMILARITY. |
| FT | DISULFID | 1633 | 1646 | BY SIMILARITY. |
| FT | DISULFID | 1652 | 1663 | BY SIMILARITY. |
| FT | DISULFID | 1658 | 1672 | BY SIMILARITY. |
| FT | DISULFID | 1674 | 1687 | BY SIMILARITY. |

Query Match 12.2% Score 171.5; DB 1; Length 2871;  
Best Local Similarity 18.9%; Pred. No. 2.1e-05;  
Matches 52; Conservative 12; Mismatches 50; Indels 161; Gaps 6;

|    |     |  |     |
|----|-----|--|-----|
| QY | 56  | RSPGLAPRPRVACCPGKRTSLPGA-----                              | 82  |
| DB | 54  | KGPVCGSRVYVACCPGKRT---LPGNQICVPICRHSCGDPGSRPMCTCPGQISPS    | 110 |
| QY | 83  | -----CGAALCPPRNGSGCVQPRCKCPA                               | 108 |
| DB | 111 | CGSRSIQHONIRCMNMGSCSDPHCLCQKGYIGTHGQPVCSGCLNGRCVAFNRCACTY  | 170 |
| QY | 109 | GWRGDTQ-----   | 116 |
| DB | 171 | GPTGQCRDRTGRCFTVVSNGMCQGLSGIVCTKLCCATVGRANGHPCMCPPAQPH     | 230 |
| QY | 117 | -----SDVDECSARRGCP-ORCVNTAGSYWCQWEGHSLSADGTLG----          | 157 |
| DB | 231 | CRGFTPIRIRGACQDVDECOAIRPMCGGNCINTVGSFECKCPAGHKFNEVSSQKCDID | 290 |
| QY | 158 | -----VPRKG-----PRVAPNPTG                                   | 172 |
| DB | 291 | ECSTIPGVCDGCECTNTVSYFCKCPGFTSPDG                           | 325 |

Search completed: December 17, 2002, 10:02:01  
Job time : 11.1935 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 17, 2002, 09:58:37 ; Search time 26.5085 Seconds  
(without alignments)  
1974.306 Million cell updates/sec

Title: US-09-852-472-3

Sequence: 1 TEHAVRPGRRVCARAHGDP.....SEQISFILEQJGSCCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP mhc:\*
- 8: SP organelle:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP viirus:\*
- 16: SP bacteriap:\*
- 17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID     | Description        |
|------------|--------|-------------|--------|-----------|--------------------|
| 1          | 1411   | 100.0       | 273    | 4 Q9UHF1  | Q9UHF1 homo sapien |
| 2          | 1410   | 99.9        | 273    | 4 Q9E6G0  | Q9E6G0 homo sapien |
| 3          | 1139.5 | 80.8        | 278    | 11 Q9GXT5 | Q9GXT5 mus musculu |
| 4          | 1063   | 75.3        | 265    | 11 Q9DCP5 | Q9DCP5 mus musculu |
| 5          | 728.5  | 51.6        | 190    | 11 Q9JMW3 | Q9JMW3 rattus norv |
| 6          | 425    | 30.1        | 293    | 11 Q35447 | Q35447 mus musculu |
| 7          | 415.5  | 29.4        | 293    | 4 Q99944  | Q99944 homo sapien |
| 8          | 276.5  | 19.6        | 509    | 5 Q9VZD0  | Q9VZD0 homo sapien |
| 9          | 276.5  | 19.6        | 512    | 5 Q9SRQ1  | Q9SRQ1 drosophila  |
| 10         | 257    | 18.2        | 1574   | 11 Q88281 | Q88281 rattus norv |
| 11         | 253.5  | 18.0        | 558    | 4 Q9UFG6  | Q9UFG6 homo sapien |
| 12         | 252.5  | 17.9        | 553    | 4 Q9NZL7  | Q9NZL7 homo sapien |
| 13         | 252.5  | 17.9        | 554    | 4 Q9N6T7  | Q9N6T7 homo sapien |
| 14         | 246.5  | 17.5        | 550    | 11 Q9JUZ5 | Q9JUZ5 mus musculu |
| 15         | 223    | 15.8        | 561    | 11 Q91V88 | Q91V88 mus musculu |
| 16         | 219    | 15.5        | 1664   | 5 Q9TVQ2  | Q9TVQ2 caenorhabdi |

|    |       |      |      |           |                    |
|----|-------|------|------|-----------|--------------------|
| 17 | 218.5 | 15.5 | 578  | 11 Q91ZD3 | Q91ZD3 mus musculu |
| 18 | 217.5 | 15.4 | 528  | 11 Q9CXD8 | Q9CXD8 mus musculu |
| 19 | 197.5 | 14.0 | 592  | 11 Q91XLS | Q91XLS mus musculu |
| 20 | 193   | 13.7 | 609  | 11 Q923T5 | Q923T5 mus musculu |
| 21 | 189   | 13.4 | 678  | 4 Q14393  | Q14393 homo sapien |
| 22 | 185.5 | 13.1 | 747  | 11 Q8VHP4 | Q8VHP4 mus musculu |
| 23 | 185.5 | 13.1 | 1034 | 11 Q8VHL7 | Q8VHL7 mus musculu |
| 24 | 184   | 13.0 | 673  | 11 Q61592 | Q61592 mus musculu |
| 25 | 184   | 13.0 | 674  | 11 Q99K57 | Q99K57 mus musculu |
| 26 | 183.5 | 13.0 | 1034 | 11 Q8VTK5 | Q8VTK5 mus musculu |
| 27 | 182.5 | 12.9 | 816  | 11 Q8R417 | Q8R417 mus musculu |
| 28 | 182   | 12.9 | 1764 | 11 Q35806 | Q35806 rattus norv |
| 29 | 181.5 | 12.9 | 815  | 4 Q96JS2  | Q96JS2 homo sapien |
| 30 | 180   | 12.8 | 2809 | 4 Q96JP8  | Q96JP8 homo sapien |
| 31 | 178.5 | 12.7 | 4555 | 11 Q8R508 | Q8R508 rattus norv |
| 32 | 178   | 12.6 | 648  | 5 Q9NKD7  | Q9NKD7 drosophila  |
| 33 | 178   | 12.6 | 674  | 11 Q63772 | Q63772 rattus sp.  |
| 34 | 178   | 12.6 | 701  | 5 Q9VUT4  | Q9VUT4 drosophila  |
| 35 | 177.5 | 12.6 | 3138 | 5 Q9VTP0  | Q9VTP0 drosophila  |
| 36 | 177   | 12.5 | 4215 | 5 Q9W332  | Q9W332 rattus norv |
| 37 | 176.5 | 12.5 | 2906 | 11 Q9WUH9 | Q9WUH9 rattus norv |
| 38 | 176   | 12.5 | 1511 | 4 Q75412  | Q75412 homo sapien |
| 39 | 175   | 12.4 | 1587 | 4 Q00508  | Q00508 homo sapien |
| 40 | 174.5 | 12.4 | 1095 | 11 Q60784 | Q60784 mus musculu |
| 41 | 174.5 | 12.4 | 3857 | 11 Q88840 | Q88840 mus musculu |
| 42 | 173.5 | 12.3 | 2872 | 11 Q9WUH8 | Q9WUH8 rattus norv |
| 43 | 172   | 12.2 | 418  | 4 Q8TF19  | Q8TF19 homo sapien |
| 44 | 172   | 12.2 | 1212 | 13 Q42347 | Q42347 gallus gall |
| 45 | 172   | 12.2 | 1833 | 11 Q08999 | Q08999 mus musculu |

ALIGNMENTS

RESULT 1  
ID Q9UHF1 PRELIMINARY; PRT; 273 AA.  
AC Q9UHF1;  
DT 01-MAY-2000 (TREMURel. 13, Created)  
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)  
DE NOTCH4-Like protein (Hypothetical 29.6 kDa protein).  
GN ZNFUI OR DKFZP586L2317.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Koehler K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL512735; CAC21666.1; -.  
DR HSSP; P08709; IPAK.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR Pfam; PF00008; EGF\_2.  
DR SMART; SM00179; EGF\_CA\_1.  
DR SMART; SM00001; EGF\_Like\_1.  
DR PROSITE; PS00010; ASX\_HYDROXYL\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA\_1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylase; Repeat.  
SQ SEQUENCE 273 AA; 29617 MW; 5740BB845ED5A988 CRC64;

Query Match 100.0%; Score 1411; DB 4; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-122;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 79  
 QY 61 APAPRYACCPGWKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCPAGWRGDTCCSDVD 120  
 DB 80 APAPRYACCPGWKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCPAGWRGDTCCSDVD 139  
 QY 121 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTCLVPKGGPRVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTCLVPKGGPRVAPNPTGVDSAMKEE 199  
 QY 181 VQRLOSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHFSFQQLGRIDSLSQISF 240  
 DB 200 VQRLOSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHFSFQQLGRIDSLSQISF 259  
 QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

## RESULT 2

Q96EGO PRELIMINARY; PRT; 273 AA.  
 AC Q96EGO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Similar to NEU1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012377; AAH12377.1; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_CA; UNKNOWN\_1.  
 SQ SEQUENCE 273 AA; 29631 MW; 5AD0A4845ED5B688 CRC64;

Query Match 99.9%; Score 1410; DB 4; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1e-121;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 79  
 QY 61 APAPRYACCPGWKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCPAGWRGDTCCSDVD 120  
 DB 80 APAPRYACCPGWKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCPAGWRGDTCCSDVD 139  
 QY 121 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTCLVPKGGPRVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTCLVPKGGPRVAPNPTGVDSAMKEE 199  
 QY 181 VQRLOSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHFSFQQLGRIDSLSQISF 240  
 DB 200 VQRLOSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHFSFQQLGRIDSLSQISF 259

QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

## RESULT 3

Q9QXT5 PRELIMINARY; PRT; 278 AA.  
 ID Q9QXT5  
 AC Q9QXT5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE NOTCH4-like protein (Vascular endothelial zinc finger 1).  
 GN VEZF1 OR ZNEU1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
 RA O'Hara P.;  
 RT "Mus musculus homolog of HLA class III region containing NOTCH4  
 gene.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
 RA Martinez T., Hoffman R., O'Hara P.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF184973; AAF01322.1; -.  
 DR EMBL; BC024610; AAH24610.1; -.  
 DR HSPF; P00740; IEDM.  
 DR MGD; MGI:1313291; Vezfl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 KW Calcium-binding; EGF-Like domain; Glycoprotein; Repeat.  
 SQ SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

Query Match 80.8%; Score 1139.5; DB 11; Length 278;  
 Best Local Similarity 79.9%; Pred. No. 7.6e-97;  
 Matches 203; Conservative 16; Mismatches 34; Indels 1; Gaps 1;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 24 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 83  
 QY 61 APAPRYACCPGWKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCPAGWRGDTCCSDVD 120  
 DB 84 TPAPRYACCPGWKRTSLGPGACGAAICQPPCGNGGSCIRFGHCRCPCVGVQGDTCQTDVD 143  
 QY 121 ECSARRGCPORCVNTAGSYWCQWEGHSLSDAGTCLVPKGGPRVAPNPTGVDSAMKEE 179  
 DB 144 ECSTGEASCPORCVNTAGSYWCQWEGQSPADGTCLSLKEGSPVAPNPTAGVDSMARE 203  
 QY 180 EYRLOSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHFSFQQLGRIDSLSQIS 239  
 DB 204 EYRLOSRVDLLEKQLVLAPLHSLASRSTEHGLQDPGSLLAHFSQQLDRIDSLSQIS 263  
 QY 240 FLEEQLGSCCKKD 253  
 DB 264 FLEEHLGSCCKKD 277



RESULT 4

09DCPS PRELIMINARY; PRT; 265 AA.  
 AC 09DCPS; PRELIMINARY; PRT; 265 AA.  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DE Vascular endothelial zinc finger 1.  
 GN VZFL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RP [1]\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RA MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shidara K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aitawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Saito T., Okazaki Y., Nishi K., Kiyosawa H., Kondo S., Yamada S.,  
 RA Kadota K., Matsuda H.A., Ashburner T., Bono H., Kasukawa T., Saito R.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehli H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,  
 RA Schirni L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio L.,  
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein S., Hill D., Hofmann M., Hume D.A., Gariboldi M.F.,  
 RA Gustincich S., Hill D., Fletcher C., Fujita M., Gariboldi M.F.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Momberti N.,  
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seza T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
 RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690 (2001).  
 DR EMBL; AK002601; BAB2222.1; -  
 DR HSSP; P00740; 1EDM.  
 DR MGD; MG1:1313291; Vexfl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF\_2.  
 DR SMART; SM00181; EGF\_2.  
 DR SMART; SM00001; EGF-like; 2.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA848FF97E CRC64;

Query Match

Best Local Similarity 75.3%; Score 1063; DB 11; Length 265;  
 Matches 192; Conservative 15; Mismatches 33; Indels 14; Gaps 2;

QY 1 TEHAYRPGRCVCAVRAHGDVSESVFQVQPELTTCDDGRACSTRTTYATYRRSGT 60  
 DB 24 TEHAYRPGRCVCAVRAHGDVSESVFQVQPELTTCDDGRACSTRTTYATYRRSGT 60  
 QY 61 AAPRRVYACCPGKRTSGLPAGCAATCOPPCNGSSCVQPRGRCPCPGMGDTCCGDDV 120  
 DB 84 TARRRYVACCPGKRTSGLPAGCAATCOPPCNGSSCVQPRGRCPCPGMGDTCCGDDV 120  
 QY 121 ECSARRGCGPCRCVNTGSGVWCOCWEGHSLADGTLCPVKGPRVAPNPT-GVDSAMKE 179  
 DB 144 ECSGTEASCPGRCVNTGSGVWCOCWEGHSLADGTLCPVKGPRVAPNPT-GVDSAMKE 179  
 QY 180 EVORLQSRVLLLEKQLVLAFLASLAQALEHGLPPGSLVHVSFOQLGRDLSLSEQIS 239  
 DB 204 EVYRLQSRVLLLEKQLVLAFLASLAQALEHGLPPGSLVHVSFOQLGRDLSLSEQIS 239  
 QY 240 FLEBQJGSCCKKD 253

Db 260 -----SCKD 264

RESULT 5

09JRW3 PRELIMINARY; PRT; 190 AA.  
 AC 09JRW3; PRELIMINARY; PRT; 190 AA.  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DE CBL20.  
 GN CBL20.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 RP [1]\_Taxid=10116;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.;  
 RT "Cloning and characterization of a novel 20.4kd Estrogen-regulated  
 protein in the Rat Spleen."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Marcantonio D., Huynh H.T.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF23678; AAF5352.1;  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF\_2.  
 DR SMART; SM00179; EGF\_2.  
 DR SMART; SM00001; EGF-like; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1B998 CRC64;

Query Match

Best Local Similarity 51.6%; Score 728.5; DB 11; Length 190;  
 Matches 131; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 86 AICOPPCNGSSCVQPRGRCPCPGMGDTCCGDDVDEGARRGCGPCRCVNTAGSYWCOW 145  
 DB 21 AICOPPCNGSSCVQPRGRCPCPGMGDTCCGDDVDEGARRGCGPCRCVNTAGSYWCOW 145  
 QY 146 EGHSLADGTLCPVKGPRVAPNPT-GVDSAMKEEYORLOSVDLLEKQLVLAFLAS 204  
 DB 81 EGOSPSADGTLCPVKGPRVAPNPT-GVDSAMKEEYORLOSVDLLEKQLVLAFLAS 204  
 QY 205 IASQALEHGLPPGSLVHVSFOQLGRDLSLSEQISFLEBQJGSCCKKD 253  
 DB 141 IASRSPHEGLQPPGSLVHVSFOQLGRDLSLSEQISFLEBQJGSCCKKD 253

RESULT 6

035447 PRELIMINARY; PRT; 293 AA.  
 AC 035447; PRELIMINARY; PRT; 293 AA.  
 DT 01-JAN-1998 (TEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
 DE Hypothetical 32.1 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RN [1]\_Taxid=10090;



RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
RA Palazon M., Peltman G.S., Pan S., Pollard D.R., Pucil J.M.,  
RA Reinert K., Remington K., Sanders R.D.C., Scheider F., Smith T.,  
RA Svirskas R., Tector C., Stappleton M., Strong R., Sun E.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yang X.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q.A.,  
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu L.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Venter H.O.,  
RT Science 287:2185-2195(2000).  
DR EMBL; AB003481; AAF47894.1; -  
DR HSSP; P00740; 1EDM.  
DR FLYbase; F8m003539; CG7447.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR00561; EGF\_1like.  
DR Pfam; PF00008; EGF\_2.  
DR SMART; SM00179; EGF\_Ca.  
DR PROSITE; PS00010; ASX\_HYDROXYL.  
DR PROSITE; PS00022; EGF\_1.  
DR PROSITE; PS01186; EGF\_2.  
DR PROSITE; PS01187; EGF\_Ca.  
DR Calcium-binding; EGF-like domain.  
SQ SEQUENCE 509 AA, 57413 MW, FE4782E4A6E121F0 CRC64;  
Query Match  
Best Local Similarity 19.6%; Score 276.5; DB 5; Length 509;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
QY 9 RVVC-AVAGADPV--SESFVQVYVOPPLTCD-----GHRACSTYRTYRYARRSFGLA 61  
DB 242 RHICMQQRTVMTVVKRTVEYSPRTWKHVAITPCOPTFSQCKTRVQVHQAAYRDVIDHK 304  
QY 62 PARP-RYACCPGKRTSGLPACGAAICQPPCRNGSCVQPCRCPCAGKRGDTCOSVD 120  
DB 302 TAQOMTYDCTCTGMSRENPBSDSCKRPICSARCQNGCCTAFTSCPTGTFGRFCQDND 364  
QY 121 ECASRGCCPCPCVNTAGSYWCCMGHSLADGTLVCPKGGPRVAPN-----P 170  
DB 362 ECQTEK-PCDQCCINTGHSIFCRQCGFVLOSQDSC-----KQVSTNADDAPEARDLE 417  
QY 171 TGVSANKEEVOPLQS-----RVDLLEKQLVLAAPLHSLASQ--ALHGLPDRG 218  
DB 415 NDIDDTDAEVAATRLQIKESLANERVHTNELQSLQATYSVVDTLKSLTLEKQADVS 477  
QY 219 SLVHSFQOLGRIDSLSQISFL 241  
DB 475 RIQTNLKYTESTINKLGMNL 497  
RESULT 9  
O88281 PRELIMINARY; PRT; 512 AA.  
AC O88281  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE L016414P.  
GN CG7447.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC NCI\_TaxID=7227;  
RN NCI\_TaxID=7227;  
SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Abhyant A., Carlson J.,  
RA Gonzalez M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Nuno J., Pacleb J., Paragas V., Park S., Miranda A., Mungall C.J.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S., Pounanavong S., Wan K.,  
DR Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY061220; RA28768.1; -  
DR FLYbase; F8m003539; CG7447.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR00561; EGF\_1like.  
DR Pfam; PF00008; EGF\_2.  
DR PROSITE; PS00010; ASX\_HYDROXYL.  
DR PROSITE; PS00022; EGF\_1.  
DR PROSITE; PS01186; EGF\_2.  
DR PROSITE; PS01187; EGF\_Ca.  
SQ SEQUENCE 512 AA, 57770 MW, 4DD372E4A6F7627 CRC64;  
Query Match  
Best Local Similarity 19.6%; Score 276.5; DB 5; Length 512;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
QY 9 RVVC-AVAGADPV--SESFVQVYVOPPLTCD-----GHRACSTYRTYRYARRSFGLA 61  
DB 245 RHICMQQRTVMTVVKRTVEYSPRTWKHVAITPCOPTFSQCKTRVQVHQAAYRDVIDHK 304  
QY 62 PARP-RYACCPGKRTSGLPACGAAICQPPCRNGSCVQPCRCPCAGKRGDTCOSVD 120  
DB 305 TAQOMTYDCTCTGMSRENPBSDSCKRPICSARCQNGCCTAFTSCPTGTFGRFCQDND 364  
QY 121 ECASRGCCPCPCVNTAGSYWCCMGHSLADGTLVCPKGGPRVAPN-----P 170  
DB 365 ECQTEK-PCDQCCINTGHSIFCRQCGFVLOSQDSC-----KQVSTNADDAPEARDLE 417  
QY 171 TGVSANKEEVOPLQS-----RVDLLEKQLVLAAPLHSLASQ--ALHGLPDRG 218  
DB 418 NDIDDTDAEVAATRLQIKESLANERVHTNELQSLQATYSVVDTLKSLTLEKQADVS 477  
QY 219 SLVHSFQOLGRIDSLSQISFL 241  
DB 478 RIQTNLKYTESTINKLGMNL 500  
RESULT 10  
O88281 PRELIMINARY; PRT; 1574 AA.  
AC O88281  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE MEGF6.  
GN MEGF6.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCI\_TaxID=10116;  
RN NCI\_TaxID=10116;  
RP SEQUENCE FROM N.A.  
RC MEDLINE=SPRAGUE-DAWLEY, TISSUE=BRAIN;  
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.,  
RT Identification of high-molecular-weight proteins with multiple EGF-  
like motifs by motif-1-trap screening";  
DR EMBL; AB011532; BA032462.1; -  
DR HSSP; P00736; 1A9Q.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR00561; EGF\_1like.  
DR Pfam; PF00008; EGF\_2.  
DR SMART; SM00179; EGF\_Ca.  
DR SMART; SM00001; EGF\_1like; 19.



DE Hypothetical 61.4 kDa protein.  
 GN W80.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1] \_TaxId=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TERATOCARCINOMA/NEURON;  
 RA Franco B.;  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TERATOCARCINOMA/NEURON;  
 RA Buchner G., Orfanelli U., Quaderni N., Bassi M.T., Andolfi G.;  
 RT "Identification of a new EGF-repeat-containing gene from human Xp22;  
 RT Acandidate for developmental disorders.";  
 CC Genomics 65:16-23(2000).  
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL: AJ245671, CAB92132.1, -.  
 DR HSSP: P00736, IAPQ.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF-like.  
 DR Pfam: PF00008, EGF\_4.  
 DR Pfam: PF00629, MAM\_1.  
 DR SMART: SM00179, EGF\_CA; 3.  
 DR SMART: SM00137, MAM\_1.  
 DR PROSITE: PS00010, ASX\_HYDROXYL, 3.  
 DR PROSITE: PS00022, EGF\_1, UNKNOWN\_1.  
 DR PROSITE: PS01186, EGF\_2, 2.  
 DR PROSITE: PS01187, EGF\_CA; 3.  
 DR PROSITE: PS50060, MAM\_2, 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 554 AA; 6138 MW; D519238P2A604101 CRC64;  
 Query Match  
 Best Local Similarity 17.9%; Score 252.5; DB 4; Length 554;  
 Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;  
 Db 39 GHRASTYRTTAYRARSFGLAPARPRYACCPGKRTSGLPACGAICOPPCRGSGC 98  
 QY 21 GNAASARHGLLSA--RQGVCHYGTKLACCYGRNS--KGYC-EATCEPCK-FGEC 74  
 Db 99 VQRCRCPCWGRGDTQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLSADGTL 158  
 QY 75 VGPVKCKCPFGYGTQSDVNECGMKRPPQHRCVNTHSGYKFCLSGHMLMPDAT-CV 133  
 QY 159 -----PKGGP-----RVAVN 169  
 Db 134 NSRTCAMINCOYSCDTEBGPCLCPSSGRLAPN 168  
 RESULT 14  
 ID Q9JUZ5 PRELIMINARY; PRT; 550 AA.  
 AC Q9JUZ5;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Hypothetical 61.5 kDa protein.  
 GN EGF6 OR W80.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1] \_TaxId=10090;  
 RP SEQUENCE FROM N.A.  
 RA Franco B.;

RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20241927; PubMed=10777661;  
 RA Buchner G., Orfanelli U., Quaderni N., Bassi M.T., Andolfi G.;  
 RT "Identification of a new EGF-repeat-containing gene from human Xp22;  
 RT Acandidate for developmental disorders.";  
 CC Genomics 65:16-23(2000).  
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL: AJ245672, CAB92138.1, -.  
 DR HSSP: P35555, IEMN.  
 DR MGD: W61:185059; EGF16.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF-like.  
 DR Pfam: PF00008, EGF\_4.  
 DR Pfam: PF00629, MAM\_1.  
 DR SMART: SM00179, EGF\_CA; 3.  
 DR SMART: SM00137, MAM\_1.  
 DR PROSITE: PS00010, ASX\_HYDROXYL, 3.  
 DR PROSITE: PS00022, EGF\_1, UNKNOWN\_1.  
 DR PROSITE: PS01186, EGF\_2, 2.  
 DR PROSITE: PS01187, EGF\_CA; 3.  
 DR PROSITE: PS50060, MAM\_2, 1.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 550 AA; 61520 MW; DE936325CF31B3 CRC64;  
 Query Match  
 Best Local Similarity 17.5%; Score 246.5; DB 11; Length 550;  
 Matches 52; Conservative 12; Mismatches 50; Indels 27; Gaps 4;  
 QY 52 TAYRSPGLAPARPRYACCPGKRTSGLPACGAICOPPCRGSGCVPQRCRCPCWGR 111  
 Db 30 SALAHQGVCGYGTGMACCYGKRN--KGYC-EATCEPCK-FGECVGPVKCKCPFGYT 85  
 QY 112 GDTCCSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLSADGTL----- 156  
 Db 86 GRTCTQDVNECGVPRCPQHRCVNTHSGYKFCLSGHMLDPATCSNRTCALNCOYGC 145  
 QY 157 -----CVPKGPPRVAVN 169  
 Db 146 EDTEGPRCVCPSSGRLAPN 166  
 RESULT 15  
 ID Q91V88 PRELIMINARY; PRT; 561 AA.  
 AC Q91V88;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE POEM (NEPHRONECTIN short isoform).  
 GN NPNT OR POEM OR NEPH1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Morimura N., Tezuka K., Watanabe N., Yasuda M., Miyatani S.,  
 RA Hozumi N., Tezuka K., Watanabe N., Yasuda M., Miyatani S.,  
 RT "Molecular cloning of POEM, A novel adhesion molecule that interacts  
 RT with alpha5beta1 integrin.";  
 RU J. Biol. Chem. 276:42172-42181(2001).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH SWISS; TISSUE=KIDNEY;  
 MEDLINE=21363579; PubMed=11470831;

US-09-852-472-3.rspt

Tue Dec 17 14:03:59 2002

Brandenberger R., Schmidt A., Linton J., Wang D., Backus C., Denda S.,

Muller U., Reichardt L.F.;

"Identification and characterization of a novel extracellular matrix

protein nephronectin that is associated with integrin alpha8beta1 in

the embryonic kidney.";

J. Cell Biol. 154:447-458 (2001).

-!- SIMILARITY: CONTAINS 1 MAM DOMAIN.

EMBL; AB059656; BAB69692.1; -

DR MGD; MGI:2148811; Npnt.

DR InterPro; IPR000152; Asx hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR000998; MAM\_domain.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00629; MAM; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_3.

DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

DR PROSITE; PS01186; EGF\_2; UNKNOWN\_3.

DR PROSITE; PS01187; EGF CA; UNKNOWN\_3.

DR PROSITE; PS00060; MAM\_2; 1.

KW Glycoprotein.

SQ SEQUENCE 561 AA; 61490 MW; 69E7ACAA0EE3F506 CRC64;

Query Match 15.8%; Score 223; DB 11; Length 561;

Best Local Similarity 43.4%; Pred. No. 3.1e-12; Indels 4; Gaps 3;

Matches 43; Conservative 12; Mismatches 40; 116

QY 57 SPGLAPARPRVACCPGKRTSLGLFCAGAAICOPPCRNNGSCVQPGRCPCPAGWGTCC 87

Db 32 SIGLCRYGGRIDCCMGWARSW--GQC-QPVCQPQKH-GEVGNKCKHPGPAKTCN 87

QY 117 SDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGT 155

Db 88 QDLNECGKPRPCPKHRCMNTFGSYKCYCLNGYMLLPDGS 126

Search completed: December 17, 2002, 10:03:02

Job time : 27.5085 secs